

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12Q 1/06, G01N 33/536, 33/543, 33/53, C07H 21/04	A1	(11) International Publication Number: WO 99/51766 (43) International Publication Date: 14 October 1999 (14.10.99)
(21) International Application Number: PCT/US99/07270 (22) International Filing Date: 2 April 1999 (02.04.99) (30) Priority Data: 09/054,936 3 April 1998 (03.04.98) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 09/054,936 (CIP) Filed on 3 April 1998 (03.04.98) (71) Applicant (for all designated States except US): INVITROGEN [US/US]; 1600 Faraday Avenue, Carlsbad, CA 92008 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): FERNANDEZ, Joseph, Manuel [US/US]; 3930 Skyline, Carlsbad, CA 92008 (US). HEYMAN, John, Alastair [US/US]; 1242B Munevar Court, Cardiff-by-the-Sea, CA 92007 (US). HOEFFLER, James, Paul [US/US]; 957 Jasmine Court, Carlsbad, CA 92009 (US). MARKS-HULL, Heather, Lynn [US/US]; 155 Hamilton Street, Oceanside, CA 92054 (US). SINDICI, Michelle, Lynn [US/US]; 418 Silvergate Avenue, San Diego, CA 92106 (US).	(74) Agent: REITER, Stephen, E.; Gray Cary Ware & Friedenrich LLP, Suite 1600, 4365 Executive Drive, San Diego, CA 92121 (US). (81) Designated States: AU, CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: METHODS FOR PRODUCING LIBRARIES OF EXPRESSIBLE GENE SEQUENCES		
(57) Abstract The present invention comprises a method for producing libraries of expressible gene sequences. The method of the invention allows for the simultaneous manipulation of multiple gene sequences and thus allows libraries to be created in an efficient and high throughput manner. The expression vectors containing verified gene sequences can be used to transfect cells for the production of recombinant proteins. The invention further comprises libraries of expressible gene sequences produced using the method of the invention and expression vectors used in the construction of said libraries.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakhstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

METHODS FOR PRODUCING LIBRARIES OF EXPRESSIBLE GENE
SEQUENCES

Field of the Invention

5 The invention disclosed herein relates to the fields of genomics and molecular biology. More specifically the invention relates to new high through-put methods of making libraries of expressed gene sequences and the libraries made using said methods.

Background of the Invention

10 Recent breakthroughs in nucleic acid sequencing technology have made possible the sequencing of entire genomes from a variety of organisms, including humans. The potential benefits of a complete genome sequence are many, ranging from applications in medicine to a greater understanding of evolutionary processes. These benefits cannot be fully realized, however, without an understanding of how
15 and where these newly sequenced genes function.

Traditionally, functional understanding started with recognizing an activity, isolating a protein associated with that activity, then identifying and isolating the gene, or genes, encoding that protein. Each gene of interest was identified, isolated and expressed separately, a relatively time consuming process.

20 Recently, breakthroughs in high through-put DNA sequencing technology have allowed massive amounts of gene sequence information to become available to the public. Yet methods of expressing these sequences to produce the proteins encoded by them for study have still required that each sequence be manipulated one at a time. Accordingly, a need exists for the development of methods for the rapid,
25 simultaneous expression of large numbers of gene sequences. The invention described herein addresses this and related needs as will become apparent upon inspection of the specification and the appended claims.

Brief Description of the Invention

The present invention comprises a method for producing libraries of expressible gene sequences. The method of the invention allows for the simultaneous manipulation of multiple gene sequences and thus allows libraries to be created in an efficient and high through-put manner. The expression vectors containing verified gene sequences can be used to transfect cells for the production of recombinant proteins. The invention method utilizes known techniques in such a way as to create an efficient high through-put means of producing libraries of expressible gene sequences.

10 The invention further comprises libraries of expressible gene sequences produced using the method of the invention and expression vectors used in the construction of such libraries.

Brief Description of the Figure

Figure 1 shows a schematic representation of the vaccinia topoisomerase type I cloning method used in the practice of the invention.

Detailed Description of the Invention

The present invention comprises a method for producing libraries of expressible gene sequences. The invention method comprises the following steps: amplifying a plurality of gene sequences, purifying the amplified gene sequences, inserting each of the purified gene sequences into an expression vector, and verifying the size and orientation of the inserted gene sequence.

In the first step, the gene sequences that are to be expressed are amplified. By "amplification" it is meant that the copy number of the gene sequence(s) is increased. One commonly used method of amplification is the polymerase chain reaction (PCR). In brief, starter DNA is heat-denatured into single strands. Two synthetic oligonucleotides, one complementary to sequence at the 3' end of the sense strand of DNA segment of interest and the other complementary to the sequence at the 3' end of

the anti-sense strand of a DNA segment of interest, are added in great excess to the DNA sequence to be amplified and the temperature is lowered to 50 - 60° C. The specific oligonucleotides hybridize with the complementary sequences in the DNA and then serve as primers of DNA chain synthesis, which requires the addition of a supply of deoxynucleotides and a temperature-resistant DNA polymerase, such as Taq polymerase, which can extend the primers at temperatures up to 72° C. When synthesis is complete, the whole mixture is heated further (up to 95° C) to melt the newly formed DNA duplexes. When the temperature is lowered again, another round of synthesis takes place, since an excess of primer is still present. Repeated cycles of synthesis and melting quickly amplify the sequence of interest. A more detailed description of PCR can be found in Erlich, Ed, *PCR Technology: Principles and Applications for DNA Amplification*, W.H. Freeman and Co., 1992 and Erlich, *et al*, Eds., *Polymerase Chain Reaction*, Cold Spring Harbor Laboratory, 1989, both of which are incorporated by reference herein.

Starter DNA can come from a variety of sources. It can be total genomic DNA from an organism, for example, or can be cDNA that has been synthesized from cellular mRNA using reverse transcriptase. Sources of suitable RNA include normal and diseased tissues, cellular extracts, and the like.

In practicing the method of the invention, the desired gene sequences can come from any source. The examples presented below show the amplification of all open reading frames (ORFs) from a single organism, *Saccharomyces cerevisiae*, for example. By "open reading frame" it is meant a segment of DNA that exists between a start codon and a stop codon and is likely to represent a gene. The examples presented below further show the amplification of a group of human genes thought to be important in the development of cancer.

Public databases exist that contain the entire or partial genome of a particular organism, for example yeast (*Saccharomyces cerevisiae*), prokaryotes (*Bacillus subtilis*, *E. coli*, *Borrelia burgdorferi*, *Helicobacter pylori*, *Mycoplasma genitalium*, and the like), fish (*Fugu rubripes*), mammals (human, mouse), plants (rice, cotton)

and the like. Well known databases include GenBank, Unigene, EMBL, IMAGE and TIGR, for example. Public databases such as these can be used a source of gene sequences for use in the method of the invention.

The primers employed in the amplification step are specific for each desired
5 gene sequence and include a variety of unique features. For example, the 5' "sense"
primer starts with the sequence 5'-CACCATG... (the start codon is underlined). The
CACC sequence is added as a Kozak consensus that aids in translational efficiency.
When the gene sequence being amplified represents a full-length gene, the 3'
"antisense" codon is preferably designed to make the amplification product end at the
10 3rd position of the last codon of the gene being amplified, plus a single adenine
residue. This facilitates the fusion of the coding region in-frame with a heterologous
peptide sequence such as an epitope tag, an affinity purification tag, and the like (see
below). The gene sequence need not encode a full-length sequence, however, as the
invention methods are equally suitable for any gene sequence, including Expressed
15 Sequence Tags (ESTs). The primers can be synthesized and dried in multiwell
formats, such as 96-well microtiter plates to facilitate identification and further
processing.

The amplified gene products are next isolated from the other components of
the amplification reaction mixture. This purification can be accomplished using a
20 variety of methodologies such as column chromatography, gel electrophoresis, and the
like. A preferred method of purification utilizes low-melt agarose gel electrophoresis.
The reaction mixture is separated and visualized by suitable means, e.g. by ethidium
bromide staining. DNA bands that represent correctly sized amplification products
are cut away from the rest of the gel and placed into appropriate corresponding wells
25 of a 96-well microtiter plate. These plugs are subsequently melted and the DNA
contained therein utilized as cloning inserts. The use of gel electrophoresis has the
advantage that the practitioner can purify the desired amplified gene sequence while
additionally verifying that the sequence is of the correct size, i.e., represents the entire
desired gene sequence.

The purified, amplified gene sequences are next inserted into an expression vector. A variety of expression vectors are suitable for use in the method of the invention, both for prokaryotic expression and eukaryotic expression. In general, the expression vector will have one or more of the following features: a promoter-
5 enhancer sequence, a selection marker sequence, an origin of replication, an affinity purification tag sequence, an inducible element sequence, an epitope-tag sequence, and the like.

Promoter-enhancer sequences are DNA sequences to which RNA polymerase binds and initiates transcription. The promoter determines the polarity of the
10 transcript by specifying which strand will be transcribed. Bacterial promoters consist of consensus sequences, -35 and -10 nucleotides relative to the transcriptional start, which are bound by a specific sigma factor and RNA polymerase. Eukaryotic promoters are more complex. Most promoters utilized in expression vectors are transcribed by RNA polymerase II. General transcription factors (GTFs) first bind
15 specific sequences near the start and then recruit the binding of RNA polymerase II. In addition to these minimal promoter elements, small sequence elements are recognized specifically by modular DNA-binding/trans-activating proteins (e.g. AP-1, SP-1) which regulate the activity of a given promoter. Viral promoters serve the same function as bacterial or eukaryotic promoters and either provide a specific RNA
20 polymerase in trans (bacteriophage T7) or recruit cellular factors and RNA polymerase (SV40, RSV, CMV). Viral promoters are preferred as they are generally particularly strong promoters.

Promoters may be, furthermore, either constitutive or, more preferably, regulatable (i.e., inducible or derepressible). Inducible elements are DNA sequence
25 elements which act in conjunction with promoters and bind either repressors (e.g. lacO/LAC Iq repressor system in *E. coli*) or inducers (e.g. gal1/GAL4 inducer system in yeast). In either case, transcription is virtually "shut off" until the promoter is derepressed or induced, at which point transcription is "turned-on".

Examples of constitutive promoters include the int promoter of bacteriophage λ , the bla promoter of the β -lactamase gene sequence of pBR322, the CAT promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left
5 promoters of bacteriophage (P_L and P_R), the trp, reca, lacZ, LacI, AraC and gal promoters of E. coli, the α -amylase (Ulmanen *et al.*, *J. Bacteriol.* 162:176-182, 1985) and the sigma-28-specific promoters of B. subtilis (Gilman *et al.*, *Gene* 132:11-20(1984)), the promoters of the bacteriophages of Bacillus (Gryczan, In: *The Molecular Biology of the Bacilli*, Academic Press, Inc., NY (1982)), Streptomyces
10 promoters (Ward *et al.*, *Mol. Gen. Genet.* 203:468-478, 1986), and the like. Exemplary prokaryotic promoters are reviewed by Glick (*J. Ind. Microbiol.* 1:277-282, 1987); Cenatiempo (*Biochimie* 68:505-516, 1986); and Gottesman (*Ann. Rev. Genet.* 18:415-442, 1984).

Preferred eukaryotic promoters include, for example, the promoter of the
15 mouse metallothionein I gene sequence (Hamer *et al.*, *J. Mol. Appl. Gen.* 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, *Cell* 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, *Nature (London)* 290:304-310, 1981); the yeast gall gene sequence promoter (Johnston *et al.*, *Proc. Natl. Acad. Sci. (USA)* 79:6971-6975, 1982); Silver *et al.*, *Proc. Natl. Acad. Sci. (USA)* 81:5951-5955,
20 1984), the CMV promoter, the EF-1 promoter, Ecdysone-responsive promoter(s), and the like.

Selection marker sequences are valuable elements in expression vectors as they provide a means to select for growth only those cells which contain a vector. Such markers are of two types: drug resistance and auxotrophic. A drug resistance
25 marker enables cells to detoxify an exogenously added drug that would otherwise kill the cell. Auxotrophic markers allow cells to synthesize an essential component (usually an amino acid) while grown in media which lacks that essential component.

Common selectable marker gene sequences include those for resistance to antibiotics such as ampicillin, tetracycline, kanamycin, streptomycin, bleomycin,

hygromycin, neomycin, Zeocin™, and the like. Selectable auxotrophic gene sequences include, for example, hisD, which allows growth in histidine free media in the presence of histidinol.

- 5 A preferred selectable marker sequence for use in yeast expression systems is URA3. Laboratory yeast strains carrying mutations in the gene which encodes orotidine-5'-phosphate decarboxylase, an enzyme essential for uracil biosynthesis, are unable to grow in the absence of exogenous uracil. A copy of the wild-type gene (ura4+ in *S. pombe* and URA3 in *S. cerevisiae*) will complement this defect in trans.

- 10 A further element useful in an expression vector is an origin of replication sequence. Replication origins are unique DNA segments that contain multiple short repeated sequences that are recognized by multimeric origin-binding proteins and which play a key role in assembling DNA replication enzymes at the origin site. Suitable origins of replication for use in expression vectors employed herein include *E. coli oriC*, 2μ and ARS (both useful in yeast systems), sf1, SV40 (useful in
15 mammalian systems), and the like.

- Additional elements that can be included in expression vectors employed in the invention method are sequences encoding affinity purification tags or epitope tags. Affinity purification tags are generally peptide sequences that can interact with a binding partner immobilized on a solid support. Synthetic DNA sequences encoding
20 multiple consecutive single amino acids, such as histidine, when fused to the expressed protein, may be used for one-step purification of the recombinant protein by high affinity binding to a resin column, such as nickel sepharose. An endopeptidase recognition sequence is often engineered between the polyamino acid tag and the protein of interest to allow subsequent removal of the leader peptide by digestion with
25 a specific protease. Sequences encoding peptides such as the chitin binding domain (which binds to chitin), glutathione-S-transferase (which binds to glutathione), biotin (which binds to avidin or strepavidin), and the like can also be used for facilitating purification of the protein of interest. The affinity purification tag can be separated

from the protein of interest by methods well known in the art, including the use of inteins (protein self-splicing elements, Chong, *et al*, *Gene* 192:271-281, 1997).

Epitope tags are short peptide sequences that are recognized by epitope specific antibodies. A fusion protein comprising a recombinant protein and an epitope tag can be simply and easily purified using an antibody bound to a chromatography resin. The presence of the epitope tag furthermore allows the recombinant protein to be detected in subsequent assays, such as Western blots, without having to produce an antibody specific for the recombinant protein itself. Examples of commonly used epitope tags include V5, glutathione-S-transferase (GST), hemagglutinin (HA), the peptide Phe-His-His-Thr-Thr, chitin binding domain, and the like.

A further useful element in an expression vector is a multiple cloning site or polylinker. Synthetic DNA encoding a series of restriction endonuclease recognition sites is inserted into a plasmid vector downstream of the promoter element. These sites are engineered for convenient cloning of DNA into the vector at a specific position.

The foregoing elements can be combined to produce expression vectors useful in the practice of the present invention. Suitable prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (for example, pBR322, ColEI, pSC101, PACYC 184, itVX, pRSET, pBAD (Invitrogen, Carlsbad, CA) and the like). Such plasmids are disclosed by Sambrook (cf. "Molecular Cloning: A Laboratory Manual", second edition, edited by Sambrook, Fritsch, & Maniatis, Cold Spring Harbor Laboratory, (1989)). *Bacillus* plasmids include pC194, pC221, pTI27, and the like, and are disclosed by Gryczan (In: *The Molecular Biology of the Bacilli*, Academic Press, NY (1982), pp. 307-329). Suitable *Streptomyces* plasmids include pJ101 (Kendall *et al.*, *J. Bacteriol.* 162:4177-4183, 1987), and streptomyces bacteriophages such as ϕ C31 (Chater *et al.*, In: *Sixth International Symposium on Actinomycetales Biology*, Akademiai Kiado, Budapest, Hungary (1986), pp. 45-54).

Pseudomonas plasmids are reviewed by John *et al.* (*Rev. Infect. Dis.* 8:693-704, 1986), and Izaki (*Jpn. J. Bacteriol.* 33:729-742, 1978).

Suitable eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, pcDNA3.1, pCDNA3.1/GS, pYES2/GS, pMT, pIND, pIND(Sp1),
5 pVgRXR (Invitrogen), and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, *Miami Wntr. Symp.* 19:265-274, 1982); Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, *Cell* 28:203-204, 1982; Dilon *et al.*, *J. Clin. Hematol. Oncol.* 10:39-48, 1980;
10 Maniatis, In: *Cell Biology: A Comprehensive Treatise*, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Construction of chimaeric DNA molecules *in vitro* relies traditionally on two enzymatic steps catalyzed by separate protein components. PCR amplification or site-specific restriction endonucleases are used to generate linear DNAs with defined
15 termini that can then be joined covalently at their ends via the action of DNA ligase. DNA ligase has limitations, however, in that it is relatively slow acting and temperature sensitive.

Thus, when inserting the purified, amplified gene sequence into the expression vector the use of an enzyme that can both cleave and religate DNA in a site specific
20 manner is preferred. Any site-specific enzyme of this type is suitable, for example, a type I topoisomerase or a site-specific recombinase. Examples of suitable site-specific recombinases include lambda integrase, FLP recombinase, P1-Cre protein, Kw recombinase, and the like (Pan, *et al.*, *J. Biol. Chem.* 268:3683-3689, 1993; Nunes-Duby, *et al.*, *EMBO J.* 13:4421-4430, 1994; Hallet and Sherratt, *FEMS Microbio. Revs* 21:157-178, 1997; Ringrose, *et al.*, *Eur J. Biochem* 248:903-912,
25 1997).

A particularly suitable enzyme for use in the invention method is a type I topoisomerase, particularly vaccinia DNA topoisomerase. Vaccinia DNA

topoisomerase binds to duplex DNA and cleaves the phosphodiester backbone of one strand. The enzyme exhibits a high level of sequence specificity, akin to that of a restriction endonuclease. Cleavage occurs at a consensus pentapyrimidine element 5'-(C/T)CCTT in the scissile strand. In the cleavage reaction, bond energy is
5 conserved via the formation of a covalent adduct between the 3' phosphate of the incised strand and a tyrosyl residue of the protein. Vaccinia topoisomerase can religate the covalently held strand across the same bond originally cleaved (as occurs during DNA relaxation) or it can religate to a heterologous acceptor DNA and thereby create a recombinant molecule.

10 When the substrate is configured such that the scissile bond is situated near (within 10 basepairs of) the 3' end of a DNA duplex, cleavage is accompanied by the spontaneous dissociation of the downstream portion of the cleaved strand. The resulting topoisomerase-DNA complex, containing a 5' single-stranded tail, can religate to an acceptor DNA if the acceptor molecule has a 5' OH tail complementary
15 to that of the activated donor complex.

In accordance with the present invention, this reaction has been optimized for joining PCR-amplified DNA fragments into plasmid vectors (See Figure 1). PCR fragments are naturally good surrogate substrates for the topoisomerase I religation step because they generally have 5' hydroxyl residues from the primers used for the
20 amplification reaction. The 5' hydroxyl is the substrate for the religation reactions. The use of vaccinia topoisomerase type I for cloning is described in detail in copending US patent application serial number 08/358,344, filed 12/19/94, incorporated by reference herein in its entirety.

The gene sequence being inserted into the expression vector can insert in
25 either the sense or antisense direction. Therefore, the invention method provides for verification of both the size and orientation of the insert to insure that the gene sequence will express the desired protein. Preferably, the insert plus vector is utilized in a standard bacterial transformation reaction and the contents of the transformation

plated onto selective growth media. Bacterial transformation and growth selection procedures are well known in the art and described in detail in, for example, Ausubel, *et al*, *Short Protocols in Molecular Biology*, 3rd ed. 1995.

Individual bacterial colonies are picked and grown in individual wells of a multiwell microtiter plate containing selective growth media. An aliquot of these cells is used directly in a diagnostic PCR reaction. Primers for this reaction are designed such that only plasmids with correctly oriented inserts give amplification product. The amplified DNA is separated and visualized by SDS-PAGE gel electrophoresis using standard protocols (see Ausubel, *et al*, *Short Protocols in Molecular Biology*, 3rd ed. 1995).

Performing the PCR reaction directly from the cultured cell lysates, rather than first preparing DNA from the bacteria, is a particular advantage of the invention method as it significantly reduces both the time needed to generate the required data and the cost of doing so.

Once plasmids containing the gene sequence insert in the correct orientation have been identified, plasmid DNA is prepared for use in the transformation of host cells for expression. Methods of preparing plasmid DNA and transformation of cells are well known to those skilled in the art. Such methods are described, for example, in Ausubel, *et al*, *supra*.

Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other organisms may also be used, including other bacterial strains.

Recognized prokaryotic hosts include bacteria such as *E. coli* and those from genera such as *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host selected for use herein must be compatible with the replicon and control sequences in the expression plasmid.

Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, and mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO, 3T3 or CHOK1, HEK 293 cells or cells of lymphoid origin (such as 32D cells) and their derivatives. Preferred mammalian host cells include nonadherent cells such as CHO, 32D, and the like. Preferred yeast host cells include *S. pombe*, *Pichia pastoris*, *S. cerevisiae* (such as INVSc1), and the like.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, nopaline synthase promoter and polyadenylation signal sequences, and the like. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase or MT promoter can be used. Rubin, *Science* 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of peptide encoded by a desired gene sequence in insect cells (Jasny, *Science* 238:1653, 1987); Miller *et al.*, In: *Genetic Engineering* (1986), Setlow, J.K., *et al.*, eds., Plenum, Vol. 8, pp. 277-297).

In a further embodiment of the invention, there are provided libraries of expressible gene sequences produced by the methods of the invention. As shown in more detail in the Examples presented below, such libraries comprise gene sequences from a variety of sources such as yeast, mammals (including humans), and the like. The present invention also features the purified, isolated or enriched versions of the expressed gene products produced by the methods described above.

Kits comprising one or more containers or vials containing components for using the libraries of the present invention are also within the scope of the invention. Kits can comprise any one or more of the following elements: one or more expressible gene sequences, cells which are or can be transfected with said gene sequences, and antibodies recognizing the expressed gene product or an epitope tag associated therewith. Cells suitable for inclusion in such a kit include bacterial cells, yeast cells (such as INVSc1), insect cells or mammalian cells (such as CHO).

In one embodiment, such a kit can comprises a detergent solution, preferably the Trax® lysing reagent (6% NP-40 and 9% Triton X-100 in 1X PBS). Also included in the kit can be one or more binding partners, *e.g.*, an antibody or antibodies, preferably a pair of antibodies to the same expressed gene product, which preferably do not compete for the same binding site on the expressed gene product.

In another embodiment, a kit can comprise more than one pair of such antibodies or other binding partners, each pair directed against a different target molecule, thus allowing the detection or measurement of a plurality of such target molecules in a sample. In a specific embodiment, one binding partner of the kit may be pre-adsorbed to a solid phase matrix, or alternatively, the binding partner and matrix are supplied separately and the attachment is performed as part of the assay procedure. The kit preferably contains the other necessary washing reagents well-known in the art. For EIA, the kit contains the chromogenic substrate as well as a reagent for stopping the enzymatic reaction when color development has occurred.

The substrate included in the kit is one appropriate for the enzyme conjugated to one of the antibody preparations. These are well-known in the art, and some are exemplified below. The kit can optionally also comprise a target molecule standard; *i.e.*, an amount of purified target molecule that is the target molecule being detected or measured.

In a specific embodiment, a kit of the invention comprises in one or more containers: (1) a solid phase carrier, such as a microtiter plate coated with a first binding partner; (2) a detectably labeled second binding partner which binds to the same expressed gene product as the first binding partner; (3) a standard sample of the expressed gene product recognized by the first and second binding partners; (4) concentrated detergent solution; and (5) optionally, diluent.

The invention will now be described in greater detail by reference to the following non-limiting examples.

Example 1 - High-throughput Expression of Yeast ORFs

The following example illustrates the creation of a library of expressible yeast gene sequences.

Amplification -

- 5 6,032 yeast ORFs and a corresponding gene-specific primer of the 3' end of each were obtained from Research Genetics (Huntsville, AL) in a 96-well microtiter plate format at a concentration of 0.3 ng/ μ l. Each gene specific primer was designed to exclude the gene's stop codon. Since the templates each contain a common sequence immediately 5' of the start ATG (5'-
- 10 GCAGTCCTGGAATTCCAGCTGACCACC) (SEQ ID NO:1), it was possible to amplify each template with a common 5' primer.

- 5 μ l of ORF template was added to a fresh 96-well microtiter plate (polycarbonate Thermowell Thinwall, Model M. Cat # 6511) using a 12 channel pipetter. 6 μ l of specific 3' primer solution (2 μ M) was added and the total volume
- 15 per well brought to 30 μ l with PCR cocktail, immediately after which the plate was placed on ice. (PCR cocktail for 120 reactions - 720 μ l 5X Buffer J, 48 μ l dNTPs (50mM stock), 12 μ l common 5' primer (1 μ g/ μ l stock), 48 μ l Taq DNA polymerase (Boeringer-Mannheim or Promega, 5 units/ μ l), 1.92 μ l Pfu DNA polymerase (Stratgene, cat. # 600153-81, 2.5 units/ μ l) and 1464 μ l distilled water. 5X Buffer J:
- 20 300 mM Tris (pH 9.5), 75 mM ammonium sulfate, 10 mM $MgCl_2$). The rubber Hybaid Micromat lid was washed by soaking in 0.1 M HCl, the rinsed for 2 minutes with distilled water and dried completely before applying to the 96-well plate.

- The PCR reaction was performed using a Hybaid, Ltd. (Middlesex, UK) thermo-cycler according to the manufacturer's instructions. The conditions used were
- 25 as follows: pre-melt step: 94° C x 4 min; melt step: 94° C x 30 sec, anneal step: 58° C x 45 sec, extend step: 72° C x 3 min - repeated for 25 cycles; final extension: 72° C x 4 min; final block temperature set to room temp (approx. 22° C). The plates were stored at 4° C.

Purification -

The plates were spun briefly at 1000 rpm, then 10 µl of 6X gel loading dye was added to each well (6X gel loading dye: 6 mM Tris (pH 8), 6 mM EDTA, 0.03% Bromphenol Blue, 30% glycerol). The entire contents of each well were loaded onto a 1% low melt agarose (Invitrogen # 46-0150) gel (plus ethidium bromide at 20 µl of a 10 mg/ml solution added to 400 mls of agarose) in 1X TAE (50X TAE = 242g Tris base, 57.1 ml glacial acetic acid, 100 ml 0.5 M EDTA, pH 8.0 per liter (water)) and run at 110 - 120 volts for 1.25 to 1.5 hours. A UV light box was used to visualize the amplification products and ensure that only correct-sized PCR products are used in the insertion step.

Insertion into expression vector(s) -

The portion of each lane containing the amplified gene sequence was cut from the gel and transferred to a well in a 96-well microtiter plate, melted on a heat block (75° C), and a portion of the melt multi-channel pipetted into a 96-well microtiter plate (7 µl/well) containing one of two expression vectors: TOPO-adapted pcDNA3.1/GS or pYES2/GS (Invitrogen, Carlsbad, CA) previously digested with HindIII. The plate was covered with parafilm and incubated at 37° C for 7 minutes. Top 10 Chemically Competent Cells (Invitrogen) were added to each well (45 µl/well, O.D.=4.7), whereupon the plate was re-covered and incubated on ice for 5 minutes. The cells were then heat shocked on a 42° C block for 1 minute and returned to ice for 1 minute. An aliquot of SOC medium was added to each well (150 µl, 20g tryptone, 5g yeast extract, 0.5g NaCl, 250 mM KCl, 20 ml 1M glucose/liter), and the plate was incubated at 37° C for 90 to 120 minutes.

The contents of each well were plated onto a LB(10g tryptone, 5g yeast extract, 10g NaCl per liter)/1.5% agar petrie plate containing the appropriate selection marker (ampicillin (50 µg/ml) for pYES2/GS and Zeocin™ (25 µg/ml) for pcDNA3.1/GS). The petrie plates were grown overnight at 37° C.

Verification of size and orientation -

Contamination is a potentially serious problem in this step. Care should be taken to guard against contaminating the process through airborne contamination, unsterile reagents or equipment, or well-to-well contamination.

- Eight colonies were picked from each petrie plate and placed in eight
- 5 individual wells of a 96-well microtiter plate. Each well contained 100 μ l of 2X LB plus 100 μ g/ml ampicillin or 50 μ g/ml Zeocin™ as appropriate for the expression vector used. The plates were incubated overnight at 37° C.

- The plates were spun briefly at 1000 rpm. The cells were stirred by pipetting up and down in a pipetter, then 2 μ l from each well was transferred to a corresponding
- 10 well in a PCR reaction plate containing 28 μ l/well PCR cocktail (PCR cocktail for 840 reactions - 5040 μ l 5X Buffer J, 336 μ l dNTPs (50mM stock), 84 μ l common 5' primer (1 μ g/ μ l stock, Dalton Chemical Lab. Inc, Ont. CAN), 84 μ l 3' H6stopprevu primer (1 μ g/ μ l, Dalton Chemical Lab. Inc, Ont. CAN), 336 μ l Taq DNA polymerase (Boeringer-Mannheim or Promega, 5 units/ μ l), and 17.64 mls distilled water.
- 15 H6stopprevu primer has the sequence 5' AAA CTC AAT GGT GAT GGT GAT GAT GACC - 3') (SEQ ID NO:2).

- The PCR reaction was run essentially as described above with the following cycle: pre-melt step: 94° C x 10 min; melt step: 94° C x 1 min, anneal step: 67° C x 1 min, extend step: 72° C x 3 min - 35 cycles; final extension: 72° C x 4 min; final
- 20 block temp set to room temp (approximately 22° C). The plates were spun briefly at 100 rpm and 6 μ l of 6X gel loading dye added to each well. Samples were run on a 1% agarose gel which was subsequently stained with ethidium bromide. Only plasmids with correctly oriented inserts give an amplification product in this step.

- The location of the positive clones was entered into a database and a
- 25 spreadsheet of positive clones generated. The spreadsheet was downloaded onto a Qiagen BioRobot 9600™ to direct the re-racking of the positive cultures into deep-

well culture blocks. Essentially, a single positive culture for each clone was grown and used to prepare plasmid DNA according to the Quia-Prep Turbo protocol.

CHO cells were transfected with the prepared plasmid DNA using the Pfx-6 PerFect Lipid system (Invitrogen, Cat #T930-16). Yeast cells (INVSc1) were
5 transfected using the S.C. EasyComp Transformation kit (Invitrogen, Cat #K5050-01). Expression was verified by Western blot using anti-V5 antibody to detect the epitope tag. A total of 558 clones expressing a correct protein were obtained after a single pass.

Example 2 - High-throughput Expression of Human Gene Sequences

10 The following example illustrates the construction of a library of expressible human gene sequences using the method of the invention. Primers were constructed based on sequences of human genes available from GenBank.

Fetal human heart tissue was obtained from the International Institute for the Advancement of Medicine (IIAM). Poly A+ mRNA was isolated using the
15 FastTrack™ 2.0 Kit (Invitrogen, Carlsbad, CA) according to the manufacturer's instructions. The mRNA was converted to first-strand cDNA using a cDNA Cycle® Kit (Invitrogen) using the oligo dT primer provided and the protocols suggested. A single cDNA synthesis reaction was split into 12 separate wells of a 96-well PCR amplification plate, and PCR amplifications were performed using specific primer
20 sets, essentially as described above, with the exception that the ratio of Taq to Pfu was 50:1 in the initial amplification (final conc. 2 U Taq:0.04 U Pfu/well).

Primers were synthesized using a Primerstation 960 (Intelligent Automation Systems, Inc.) used according to the manufacturer's instructions and were designed from sequences downloaded from Unigene and sent directly to the synthesizer.
25 Approximately 15 nMoles of each primer, having an average length of 25 basepairs, was synthesized in a 96-well format. After synthesis, the primers were cleaved from the supports, deprotected and dried in the same 96-well format (see manufacturer's instructions).

The amplified gene sequences were purified and inserted into the pcDNA3.1/GS expression vector essentially as described above. The expression vectors containing sequences verified to be in the correct orientation were transfected into CHO cells in 96-well deep-well blocks using the Pfx-6 PerFect Lipid system (Invitrogen, Cat #T930-16). Cell lysates were made 48 hours after transfection, and the lysates were separated by SDS-PAGE and analyzed by Western blot according to standard protocols using an anti-V5 epitope tag Mab/horseradish peroxidase conjugate. Table 1 lists the human proteins successfully expressed using this methodology. A total of 66 clones expressing a correct protein, out of 118, were obtained after a single pass.

Table 1 - Human ORFs

Plate Number	Accession Number	Description	Predicted Size	Actual Size
M235 C7	H-A06977	albumin	67.1	67.0kDa
E1	H-AB002391	Human mRNA for KIAA0393 gene, complete cds	68.09	68
H3	H-AB006969	Homo sapiens hGAA1 mRNA, complete cds	68.42	70
E2	H-AB007875	Homo sapiens KIAA0415 mRNA, complete cds	51.48	51
D1	H-AB007887	Homo sapiens KIAA0427 mRNA, complete cds	66.55	70
M421 D6	H-AB010710	Homo sapiens mRNA for lectin-like oxidized LDL receptor, complete cds	30.14	45.0kDa
G3	H-AD001528	Homo sapiens spermidine aminopropyltransferase mRNA, complete cds	40.37	40
B5	H-AE000659	Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the C	12.39	16
E2	H-AF004022	Homo sapiens protein kinase mRNA, complete cds	38.28	44
M428 C1	H-AF004231	Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds	65.78	70.0kDa
A5	H-AF004327	Homo sapiens angiopoietin-2 mRNA, complete cds	54.67	60
C1	H-AF006501	Homo sapiens chromosome 22 cosmid clone c1155, RNA polymerase II subunit 14.4 kDa (POLRF) gene, complete cds	14.08	24

H4	H-AF008936	Homo sapiens syntaxin-16B mRNA, complete cds	35.75	47
H5	H-AF009243	Homo sapiens proline-rich Gla protein 2 (PRGP2) mRNA, complete cds	22.33	36
M462 D6	H-AF013249	Homo sapiens leukocyte-associated Ig-like receptor-1 (LAIR-1) mRNA, complete cds	31.68	40.0kDa
A1	H-AF013512	untitled	53.02	53
A3	H-AF013970	Homo sapiens MTG8-like protein (MTGR1) mRNA, complete cds	66.55	70
M467 A7	H-AF014807	Homo sapiens phosphatidylinositol synthase (PIS) mRNA, complete cds	23.54	29.0kDa
D2	H-AF015257	Homo sapiens flow-induced endothelial G protein-coupled receptor (FEG-1) mRNA, complete cds	41.36	40
M422 B5	H-AF017307	Homo sapiens Ets-related transcription factor (ERT) mRNA, complete cds	40.92	49.0kDa
A6	H-AF017656	Homo sapiens G protein beta 5 subunit mRNA, complete cds	38.94	48
E1	H-AF017995	Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDK1) mRNA, complete cds	61.27	52
G1	H-AF019612	Homo sapiens S2P mRNA, complete cds	57.2	57
D3	H-AF020591	Homo sapiens zinc finger protein mRNA, complete cds	78.76	74
A7	H-AF022385	Homo sapiens apoptosis-related protein TFAR15 (TFAR15) mRNA, complete cds	23.43	33
H6	H-AF024714	Homo sapiens interferon-inducible protein (AIM2) mRNA, complete cds	37.84	48
B1	H-AF025527	Homo sapiens leucocyte immunoglobulin-like receptor-4 (LIR-4) mRNA, complete cds	48.4	47
M424 B4	H-AF025532	Homo sapiens leucocyte immunoglobulin-like receptor-5 (LIR-5) mRNA, complete cds	49.39	59.0kDa
H5	H-AF026071	Homo sapiens soluble death receptor 3 beta (DR3) mRNA, complete cds	30.58	50
M428 A1	H-AF026273	Homo sapiens interleukin-1 receptor-associated kinase-2 mRNA, complete cds	65.01	68.0kDa
B6	H-AF026293	Homo sapiens chaperonin containing t-complex polypeptide 1, beta subunit (Cctb) mRNA, complete cds	58.96	58

B5	H-AF026548	Homo sapiens branched chain alpha-ketoacid dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds	45.43	50
B2	H-AF027204	Homo sapiens putative tetraspan transmembrane protein L6H (TM4SF5) mRNA, complete cds	21.78	27
M426 D3	H-AF028008	Homo sapiens SP1-like zinc finger transcription factor SLP mRNA, complete cds	56.43	64.0kDa
B1	H-AF029232	Homo sapiens calpamodulin (CalpM) mRNA, complete cds	70.62	70
M422 A7	H-AF029761	Homo sapiens decoy receptor 2 mRNA, complete cds	42.57	50.0kDa
M477 F3	H-AF029893	Homo sapiens i-beta-1,3-N-acetylglucosaminyltransferase mRNA, complete cds	45.76	50.0kDa
C5	H-AF032437	Homo sapiens mitogen activated protein kinase activated protein kinase gene, complete cds	51.92	50
M416 F3	H-AF035824	Homo sapiens vesicle soluble NSF attachment protein receptor (VTI1) mRNA, complete cds	25.63	36.0kDa
F3	H-AF037335	Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds	39.05	39
G1	H-AF039019	Homo sapiens zinc finger DNA binding protein 89 kDa (ZBP-89) mRNA, complete cds	87.45	87
G1	H-AF039136	Homo sapiens Fas binding protein (hDaxx) mRNA, complete cds	81.51	98
A7	H-AF040705	Homo sapiens putative tumor suppressor protein unspliced form (Fus-2) mRNA, complete cds	31.57	41
M469 F1	H-AF040958	Homo sapiens lysosomal neuraminidase precursor, mRNA, complete cds	45.76	46.0kDa
G2	H-AF043472	Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (Kv9.3) mRNA, complete cds	54.12	64
E2	H-AJ001340	Homo sapiens mRNA for U3 snoRNP associated 55 kDa protein	52.36	60
G1	H-D00096	Transtyretin (prealbumin)	16.28	20
C4	H-D00408	Cytochrome P450 IIIA7 (P450-HFLa)	55.44	64
M302 E7	H-D00682	cofilin	18.37	30
M383 G2	H-D00726	ferrochelatase	46.64	50.0kDa
M383 C3	H-D00760	proteasome, subunit HC3	25.85	34.0kDa
M305 B4	H-D00761	proteasome, subunit HC5	26.62	33
M266 F7	H-D00763	proteasome, subunit HC9	28.82	33

E2	H-D00860	Phosphoribosyl pyrophosphate synthetase subunit I	35.09	47
215-13	H-D10522	human mRNA for 80K-L protein	35	36.59
M423 F5	H-D11086	Interleukin 2 receptor gamma chain	40.7	45.0kDa
M248 D2	H-D11094	positive modulator of HIV tat-mediated transactivation	47.74	40.0kDa
G3	H-D11428	Peripheral myelin protein 22	17.71	17
M424 D3	H-D13168	Human gene for endothelin-B receptor (hET-BR)	48.73	48.0kDa
M271 B8	H-D13315	glyoxalase I, LACTOYLGLUTATHIONE LYASE. CATALYZES THE CONVERSION OF HEMIMERCAPTAL, FORMED FROM METHYLGLYOXAL AND GLUTATHIONE, TO S-LACTOYLGLUTATHIONE.	20.35	34.0kDa
M306 F1	H-D13627	hypothetical protein (GB:D13627)	60.39	90
M248 D1	H-D13630	hypothetical protein (GB:D13630) , Human mRNA for KIAA0005 gene, complete cds	46.2	49
M270 D5	H-D13634	hypothetical protein (GB:D13634)	34.65	42.0kDa
M250 D2	H-D13642	hypothetical protein (GB:D13642), Human mRNA for KIAA0017 gene, complete cds	44	48.0kDa
M250 E6	H-D13748	translation initiation factor 4A	44.77	49.0kDa
M305 C3	H-D13892	carboxyl methyltransferase, aspartate	25.19	34
D1	H-D13900	enoyl-Coenzyme A hydratase, short chain, mitochondrial	32.01	58
E1	H-D14446	Human HFREP-1 mRNA for unknown protein, complete cds	34.43	40
167-14	H-D14497	H.sapiens (Ewing's sarcoma cell line) mRNA encoding open reading frame	51.44	64
M266 D2	H-D14520	basic transcription element-binding protein 2	24.2	33.0kDa
M318 D2	H-D14658	hypothetical protein (GB:D14658)	13.64	17
D2	H-D14661	Human mRNA for KIAA0105 gene, complete cds	16.72	28
M236 E2	H-D14662	HYPOTHETICAL 29.5 KD PROTEIN IN UBP13-KIP1 INTERGENIC REGION [Saccharomyces cerevisiae]	24.75	36.0kDa
M271 G6	H-D14695	hypothetical protein (GB:D14695), Human mRNA for KIAA0025 gene, complete cds.	43.12	50.0kDa
M311 A3	H-D14696	hypothetical protein (GB:D14696)	25.74	30.0kDa

H3	H-D14697	Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)	46.2	55
M271 E7	H-D14705	catenin, alpha 2(E). Catenin (cadherin-associated protein), alpha 1 (102kD). ASSOCIATES WITH THE CYTOPLASMIC DOMAIN OF A VARIETY OF CADHERINS.	99.77	110
M236 A6	H-D14811	hypothetical protein (GB:D14811)	30.25	42
M250 A3	H-D14812	hypothetical protein (GB:D14812), Human mRNA for KIAA0026 gene, complete cds		
A5	H-D14874	Human mRNA for adrenomedullin, complete cds	20.46	33
F3	H-D14887	Human mRNA for TFIIA-42, complete cds	41.47	50
M250 H6	H-D16234	phospholipase C, alpha , PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR [Homo sapiens]	55.66	56.0kDa
M305 B1	H-D16480	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase trifunctional protein, alpha-subunit, mitochondrial	84.04	84
M271 G2	H-D16481	3-ketoacyl-CoA thiolase, beta subunit, mitochondrial, Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit		
H1	H-D16626	Histidine ammonia-lyase	72.38	64
A2	H-D17532	Human mRNA for RCK, complete cds	52.03	53
M266 F4	H-D17554	DNA-binding protein TAX	31.79	38
M248 A3	H-D21235	xeroderma pigmentosum group C repair complementing protein HHR23A	40.04	55
M235 E1	H-D21261	SM22-ALPHA HOMOLOG, hypothetical protein (GB:D21261)	22	31
M311 E1	H-D21262	hypothetical protein (GB:D21262)	77.950	63
M466 B4	H-D21853	Human mRNA for KIAA0111 gene, complete cds	45.32	49.0kDa
M311 H3	H-D23660	ribosomal protein L4	47.08	47
M419 E1	H-D26309	human mRNA for LIMK (LIM kinase)	71.240	75.0kDa

M271 B9	H-D26362	hypothetical protein (GB:D26362), Human mRNA for KIAA0043 gene, complete cds	79.97	70
M361 H2	H-D26598	proteasome, subunit HsC10-II	22.66	33.0kDa
M302 G4	H-D26599	proteasome, subunit HsC7-I	22.22	34
G1	H-D26600	Human mRNA for proteasome subunit HsN3, complete cds	29.15	36
G9	H-D28540	hypothetical protein, CDC10 homolog	44.77	60
M266 A5	H-D29011	proteasome, subunit X	22.99	23
M236 F3	H-D29012	Proteasome (prosome, macropain) delta subunit, beta type, 6	26.4	32.0kDa
C1	H-D30037	Human mRNA for phosphatidylinositol transfer protein (PI-TPbeta), complete cds	29.92	38
M250 H4	H-D30655	translation initiation factor 4AII, and ribosomal binding protein	44.88	45.0kDa
167-26	H-D30742	human mRNA for calmodulin-dependent protein kinase IV	52.10	55
M236 A4	H-D31767	hypothetical protein (GB:D31767), Human mRNA for KIAA0058 gene, complete cds	18.59	30
E1	H-D31883	Human mRNA for KIAA0059 gene, complete cds	50.93	64
G2	H-D32129	MHC class I protein HLA-A	40.26	50
M422 A6	H-D37965	Human mRNA for PDGF receptor beta-like tumor suppressor (PRLTS), complete cds	41.36	45.0kDa
M305 H4	H-D38047	26S proteasome regulatory subunit P31	28.340	34.0kDa
M423 B2	H-D38081	Thromboxane A2 receptor	37.84	45.0kDa
M317 D3	H-D38305	ErbB-2 transducer	38.06	49
M270 A8	H-D38583	calcizzarin, Human mRNA for calcizzarin, complete cds	11.66	12
M270 A6	H-D42038	hypothetical protein (GB:D42038), Human mRNA for KIAA0087 gene, complete cds	15.29	27
M318 F3	H-D42085	hypothetical protein (GB:D42085)	90.2	100
M311 C2	H-D43642	YL-1 protein homolog	40.15	36
E1	H-D45213	Human mRNA for zinc finger protein, complete cds	12.87	20
M236 B2	H-D45248	proteasome activator hPA28, subunit beta, may be cell adhesion protein	26.4	38
H3	H-D45887	Human mRNA for calmodulin, complete cds	16.5	20
166-3	H-D45906	human mRNA for LIMK-2	70	70.25
A7	H-D49357	Human mRNA for S-adenosylmethionine synthetase, complete cds	43.56	51
C5	H-D49489	Human mRNA for protein disulfide isomerase-related protein P5, complete cds	48.51	54

M482 E2	H-D49958	Human fetus brain mRNA for membrane glycoprotein M6, complete cds	30.69	32.0kDa
M305 G5	H-D50063	proteasome, subunit p40	35.75	39
M250 B6	H-D50310	cyclin I, Human mRNA for cyclin I, complete cds	41.58	47
E3	H-D50419	Homo sapiens mRNA for OTK18, complete cds	78.32	64
M298 B1	H-D50495	transcription elongation factor h-SII-T1 (GB:D50495)	33	33.0kDa
M302 A3	H-D50840	ceramide glucosyltransferase	43.45	44
167-40	H-D50863	human mRNA for TESK1	68.9 3	70
166-28	H-D50927	human myeloblast mRNA for KIAA0137 gene	60.46	64
D1	H-D63521	Homo sapiens mRNA for LECT2 precursor, complete cds	16.72	16
M302 A5	H-D78134	glycine-rich binding protein CIRP	19.03	30.0kDa
M313 E5	H-D78275	proteasome subunit p42	42.9	48.0kDa
B3	H-D79205	Human mRNA for ribosomal protein L39, complete cds	5.72	10
A4	H-D79206	Human gene for ryudocan core protein, exon1-5, complete cds	21.89	33
A1	H-D80008	Human mRNA for KIAA0186 gene, complete cds	21.67	32
M298 H4	H-D83004	ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product	16.83	32.0kDa
C3	H-D83702	Human brain mRNA for photolyase homolog, complete cds	64.57	64
M306 A1	H-D83735	neutral calponin	34.1	34.0kDa
H2	H-D86322	Homo sapiens mRNA for calmegin, complete cds	67.21	64
B1	H-D86979	Human mRNA for KIAA0226 gene, complete cds	82.72	82
169-16	H-D87116	dual specificity mitogen-activated protein kinase kinase 3	38.24	42
166-27	H-D87119	human cancellous bone osteoblast mRNA for GS3955	37.80	40
E2	H-D88308	Homo sapiens mRNA for very-long-chain acyl-CoA synthetase, complete cds	68.31	64
166-26	H-D89077	human mRNA for Src-like adapter protein	30.43	38
M440 H2	H-D89479	Homo sapiens mRNA for ST1B2, complete cds	32.67	38.0kDa
H1	H-D90086	Human pyruvate dehydrogenase (EC 1.2.4.1) beta subunit gene, exons 1-10	39.6	35
M362 F1	H-D90209	DNA-binding protein TAXREB67	38.72	48.0kDa
M316 B2	H-J00068	actin, alpha 1, skeletal muscle	41.58	50
M250 B2	H-J00194	major histocompatibility complex, MHC class II, DR alpha	28.05	36.0kDa

G2	H-J00212	Interferon, alpha 21	20.9	30
G1	H-J00287	Human pepsinogen gene	42.79	48
M298 C2	H-J02611	apolipoprotein D	20.9	31.0kDa
M266 C4	H-J02683	ADP/ATP carrier protein	32.89	36
M383 H2	H-J02685	plasminogen activator inhibitor, placenta	45.76	50.0kDa
167-3	H-J02853	"casein kinase II, alpha chain"	43.08	50
E3	H-J02854	Human 20-kDa myosin light chain (MLC-2) mRNA, complete cds	19.03	31
M248 F3	H-J02874	fatty-acid-binding protein 4, adipocyte, LIPID TRANSPORT PROTEIN IN ADIPOCYTES	14.63	17
M235 D5	H-J02939	antigen 4F2, heavy chain	58.3	58
C3	H-J02943	Corticosteroid binding globulin	44.66	50
M248 F2	H-J02966	adenine nucleotide translocator 1 (skeletal muscle) [ANT1], CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.	32.78	33
E1	H-J02982	Glycophorin B	10.12	20
167-91	H-J03075	"protein kinase c substrate, 80 kD protein heavy chain"	58.04	98
M266 A3	H-J03191	profilin 1	15.51	17.0kDa
M248 H4	H-J03231	glucose-6-phosphate dehydrogenase [G6PD]	56.76	51
M266 F2	H-J03459	LEUKOTRIENE A-4 HYDROLASE [Homo sapiens]	67.32	64
A2	H-J03460	Prolactin-induced protein	16.17	26
M271 E5	H-J03799	laminin receptor 1, Laminin receptor (2H5 epitope). 40S RIBOSOMAL PROTEIN SA [Homo sapiens].	32.56	
M440 A4	H-J03890	Human pulmonary surfactant protein C (SP-C) and pulmonary surfactant protein C1 (SP-C1) genes, complete cds	21.78	30.0kDa
M271 D8	H-J03934	NAD(P)H menadione oxidoreductase 1, dioxin-inducible. INVOLVED IN DETOXICATION PATHWAYS.	30.25	38
M271 A8	H-J04031	trifunctional enzyme (GB:J04031). C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC [Homo sapiens]	102.96	117.0kDa
M305 F6	H-J04046	calmodulin 3 [CALM3]	16.5	20
M305 G7	H-J04071	cytotoxic T-lymphocyte-associated serine esterase 1 (cathepsin G-like 1, granzyme B) [CTLA1]	27.28	38
M311 D2	H-J04183	lysosomal-associated membrane protein 2	44.99	47

M300 F4	H-J04205	Sjogren syndrome antigen B	44.99	51.0kDa
M416 G8	H-J04430	Acid phosphatase 5, tartrate resistant	35.64	45.0kDa
B1	H-J04501	Glycogen synthase 1 (muscle)	81.18	81
M313 B5	H-J04543	synexin	51.37	51
B1	H-J04605	Peptidase D	54.34	55
M250 C6	H-J04615	small nuclear ribonucleoprotein SM-D, ROLE IN THE PRE-mRNA SPLICING OR IN SNRNPSTRUCTURE.	26.51	34.0kDa
M248 E2	H-J04964	steroid sulfatase (microsomal) [STS]	64.24	60.0kDa
M250 A7	H-J05249	replication protein A, 32 kDa subunit, REQUIRED FOR SV 40 DNA REPLICATION IN VITRO, RP-A IS SINGLE-STRANDED DNA-BINDING PROTEIN.	29.81	36.0kDa
F1	H-J05272	IMP (inosine monophosphate) dehydrogenase 1	56.65	51
169-15	H-J05401	"creatine kinase, sarcomeric mitochondrial precursor"	50	46.16
M266 E4	H-J05448	RNA polymerase II, subunit B33	30.36	35.0kDa
M305 C2	H-K00558	tubulin, alpha k1 [TUBA*]	49.72	52.0kDa
M416 H7	H-K01571	Human T-cell receptor active beta-chain, mRNA from cell line MOLT-3, complete cds	34.43	36.0kDa
M311 E4	H-K01763	haptoglobin	38.28	47.0kDa
G5	H-K02100	Human ornithine transcarbamylase (OTC) mRNA, complete coding sequence	39.05	47
M302 D5	H-K02574	purine nucleoside phosphorylase	31.9	36.0kDa
169-39	H-K02581	"thymidine kinase, cytosolic"	34	25.81
M248 E4	H-K03020	phenylalanine hydroxylase [PAH]	49.83	50
M556 B3	H-K03191	Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1	56.43	53.0kDa
H2	H-L00190	Antithrombin III	51.15	55
169-62	H-L01087	"protein kinase c, theta type"	80	77.7
M318 C2	H-L01124	ribosomal protein S13	16.72	28
M313 F1	H-L02321	glutathione S-transferase M5	24.09	28
M305 E5	H-L02426	protease 26S, regulatory subunit 4	48.51	53
M302 D4	H-L02547	cleavage stimulation factor, 50 kDa subunit	47.52	50.0kDa
M266 H7	H-L02648	transcobalamin II	47.08	48.0kDa
E2	H-L02932	Human peroxisome proliferator activated receptor mRNA, complete cds	51.59	59
M270 A1	H-L03380	gonadotropin-releasing hormone receptor [GRHR], THIS RECEPTOR MEDIATES ITS ACTION BY ASSOCIATION WITH G PROTEINS	36.19	36

M270 H1	H-L03411	RD protein [RDBP], Radin blood group	41.91	59.0kDa
D3	H-L03426	Human XE7 mRNA, complete alternate coding regions	42.46	45
B1	H-L03785	Myosin, light polypeptide 5, regulatory	19.14	32
A7	H-L04483	ribosomal protein S21	9.24	34
M416 B2	H-L05147	Human dual specificity phosphatase tyrosine/serine mRNA, complete cds	20.46	30.0kDa
215-38	H-L05624	dual specificity mitogen-activated protein kinase kinase 1	50	43.30
M271 D4	H-L06132	anion channel, voltage-gated, isoform 1. FORMS A CHANNEL THROUGH THE CELL MEMBRANE, THAT ALLOWS DIFFUSION FROM SMALL HYDROPHYLIC MOLECULES.	31.24	37
169-27	H-L06139	tyrosine-protein kinase receptor TIE-2 precursor	125	123.7
H1	H-L06147	Human (clone SY11) golgin-95 mRNA, complete cds	68.31	68
M250 A1	H-L06419	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) [PLOD]	80.08	80.0kDa
M236 F6	H-L06498	ribosomal protein S20	13.2	23.0kDa
M318 D1	H-L06499	ribosomal protein L37a	10.23	27
M270 D1	H-L07414	CD40 antigen ligand [CD40LG], INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.	28.82	36
M298 A6	H-L07548	aminoacylase 1	44.99	52.0kDa
M424 C3	H-L07592	Human peroxisome proliferator activated receptor mRNA, complete cds	48.62	48.0kDa
M298 G6	H-L07633	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) [PSME1]	27.5	33.0kDa
M318 B1	H-L08096	CD70 antigen (CD27 ligand) [CD70]	21.34	28
D2	H-L08187	cytokine receptor EBI3	25.3	42
M313 F4	H-L08850	amyloid, non-A beta component, Alzheimer's disease	15.51	31.0kDa
M426 E1	H-L08895	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	52.14	60.0kDa
M266 A8	H-L09235	ATPase, vacuolar	67.98	64.0kDa
M266 D1	H-L09604	differentiation-dependent intestinal membrane A4 protein (Homo sapiens)	16.83	17.0kDa
M317 C1	H-L10338	sodium channel, voltage-gated, type I, beta polypeptide [SCN1B]	24.09	24
M317 E1	H-L10717	tyrosine-protein kinase ITK/TSK	68.270	68.0kDa
M300 B5	H-L10820	formyl peptide receptor 1 [FPR1]	38.61	37

M312 A4	H-L10838	pre-mRNA splicing factor SRp20	18.15	31.0kDa
M300 A5	H-L10918	chemokine (C-C) receptor 1 [CMKBR1]	39.16	30
M311 F2	H-L11245	complement component 4-binding protein, beta	27.83	30
M266 B7	H-L11353	neurofibromatosis 2 (bilateral acoustic neuroma) [NF2]	65.56	63.0kDa
M311 B3	H-L11667	cyclophilin 40	40.81	50.0kDa
215-49	H-L11695	serine/threonine-protein kinase receptor R4 precursor	64	55.40
M466 C2	H-L11931	Human cytosolic serine hydroxymethyltransferase (SHMT) mRNA, complete cds	53.24	56.0kDa
M271 B7	H-L12168	ADENYLYL CYCLASE- ASSOCIATED PROTEIN 1 [Homo sapiens]	52.36	60.0kDa
M416 D4	H-L12964	Interleukin-activated receptor, homolog of mouse Ly63	28.16	38.0kDa
B3	H-L13203	Human HNF-3/fork-head homolog-3 HFH-3 mRNA, complete cds	38.72	49
D2	H-L13744	Human AF-9 mRNA, complete cds	62.59	63
167-8	H-L13943	glycerol kinase	60	57.71
M311 G3	H-L13974	leucine zipper protein (GB:L13974)	41.14	51
M271 H5	H-L13977	LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR [Homo sapiens].	54.67	57
M270 G2	H-L14283	protein kinase C, zeta [PRKCZ], SERINE- AND THREONINE- SPECIFIC ENZYME.	65.23	98
M235 A3	H-L14286	antioxidant protein, thiol-specific	21.89	32.0kDa
M426 H3	H-L14778	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha){alternative products}	57.42	60.0kDa
B4	H-L15702	complement factor B	84.15	100
M426 A4	H-L16794	Human transcription factor (MEF2) mRNA, complete cds	57.42	60.0kDa
215-25	H-L16862	g protein-coupled receptor kinase GRK6	70	63.4
167-74	H-L16991	thymidylate kinase	36	23.39
169-3	H-L18964	"protein kinase c, iota type"	80	64.64
M305 E2	H-L18972	hypothetical protein (GB:L18972)	75.24	78
M426 D4	H-L19067	Human NF-kappa-B transcription factor p65 subunit mRNA, complete cds	59.18	63.0kDa
215-26	H-L19268	Homo sapiens myotonic dystrophy associated protein kinase mRNA	70	68.71

M271 E1	H-L19297	carbonic anhydrase V [CA5], Mitochondrial carbonic anhydrase. REVERSIBLE HYDRATATION OF CARBON DIOXIDE.	33.66	42
M298 G4	H-L19437	transaldolase	37.18	39.0kDa
M423 C4	H-L19593	Interleukin 8 receptor, beta	39.71	41.0kDa
G1	H-L19686	Homo sapiens macrophage migration inhibitory factor (MIF) gene, complete cds	12.76	13
G2	H-L19739	metallopanstimulin 1	9.35	32
M302 E3	H-L19871	activating transcription factor 3	20.02	36.0kDa
167-86	H-L20422	14-3-3 protein eta	34	27.1 3
M440 B2	H-L20492	Human gamma-glutamyl transpeptidase mRNA, complete cds	24.86	35.0kDa
M315 B1	H-L20688	GDP-dissociation inhibitor protein rhoA	22.22	32
M271 H3	H-L20941	ferritin, heavy polypeptide. FERRITIN IS AN INTRACELLULAR MOLECULE THAT STORES IRON IN A SOLUBLE, NONTOXIC, READILY AVAILABLE FORM.	20.24	32
M235 B7	H-L21893	Na+/taurocholate cotransporter, STRICTLY DEPENDENT ON THE		
F1	H-L21934	Sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase)	60.61	60
C2	H-L22075	Human guanine nucleotide regulatory protein (G13) mRNA, complete cds	41.58	50
169-18	H-L22206	vasopressin v2 receptor	60	58.00
M421 A10	H-L22214	Human adenosine A1 receptor (ADORA1) mRNA exons 1-6, complete cds	35.97	38.0kDa
M424 F1	H-L23959	Homo sapiens E2F-related transcription factor (DP-1) mRNA, complete cds	45.21	53.0kDa
C2	H-L24498	Human gadd45 gene, complete cds	18.26	28
M302 E2	H-L25080	proto-oncogene rhoA, multidrug resistance protein	21.34	31
M270 B8	H-L25081	guanine nucleotide-binding and transforming protein rhoC, Aplysia ras-related homolog 9	21.34	30
M236 E3	H-L25085	Sec61 complex, beta subunit, PROTEIN TRANSLOCATION IN THE ENDOPLASMIC RETICULUM	10.67	19
167-85	H-L25610	cyclin-dependent kinase inhibitor 1	32	18.11

B2	H-L25610	cyclin-dependent kinase inhibitor 1	18.110	40
M297 H2	H-L26232	cathepsin A/phospholipid transfer protein	54.34	64.0kDa
167-4	H-L26318	stress-activated protein kinase JNK1	52	42.31
M428 F1	H-L27586	Human TR4 orphan receptor mRNA, complete cds	67.76	67.0kDa
M302 E5	H-L27711	protein phosphatase KAP1	23.43	28
M250 A6	H-L28010	Homo sapiens HnRNP F protein mRNA, complete cds,		
F1	H-L28821	Alpha mannosidase II isozyme	87.67	87
167-89	H-L28824	tyrosine-protein kinase SYK	70	69.92
M298 E6	H-L28997	ADP-ribosylation factor-like gene 1	20.02	33.0kDa
D4	H-L29219	Homo sapiens clk1 mRNA, complete cds	53.35	60
169-63	H-L29222	Homo sapiens clk1 mRNA	25	15.0 3
M429 B3	H-L29277	Signal transducer and activator of transcription 3 (acute-phase response factor)	84.81	88.0kDa
C1	H-L29433	Human factor X (blood coagulation factor) gene	53.79	64
G3	H-L31860	Glycophorin A	16.61	26
D1	H-L31881	Nuclear factor I/X (CCAAT-binding transcription factor)	48.62	48
169-13	H-L31951	human protein kinase (JNK2) mRNA	55	46.71
A1	H-L32179	Arylacetamide deacetylase (esterase)	44	50
B2	H-L33404	Human stratum corneum chymotryptic enzyme mRNA, complete cds	27.94	36
M312 D3	H-L33799	procollagen C-proteinase enhancer	49.5	51.0kDa
169-77	H-L33801	human protein kinase mRNA GSK-3	55	46.27
M305 D6	H-L34041	L-glycerol-3-phosphate:NAD+ oxidoreductase	38.5	42.0kDa
B4	H-L34355	Homo sapiens (clone p4) 50 kD dystrophin-associated glycoprotein mRNA, complete cds	42.68	47
M297 B3	H-L35013	spliceosomal protein SAP 49	46.75	52.0kDa
167-32	H-L35253	human CSaids binding protein (CSBP1) mRNA	52	39.67
M266 D6	H-L35545	C/activated protein C receptor, endothelial	26.29	38.0kDa
M300 F1	H-L35594	autotaxin	100.76	91.0kDa
M318 E2	H-L36720	bystin	33.77	29
M305 H2	H-L37127	RNA polymerase II	12.98	16
M300 D1	H-L38490	ADP-ribosylation factor (GB:L38490)	22.22	32

M318 E1	H-L38941	ribosomal protein L34	12.98	18
C2	H-L38969	Homo sapiens thrombospondin 3 (THBS3) gene, complete cds	105.27	110
M476 F4	H-L39060	Homo sapiens transcription factor SL1 mRNA, complete cds	49.61	53.0kDa
M300 E4	H-L40399	hypothetical protein (GB:L40399)	29.26	36
E3	H-L40802	Homo sapiens 17-beta-hydroxysteroid dehydrogenase (17-HSD) gene	42.68	60
M478 F1	H-L40904	H. sapiens peroxisome proliferator activated receptor gamma, complete cds	52.69	60.0kDa
M306 C2	H-L41268	natural killer associated transcript 2 [NKAT2*]	37.62	40
M306 E2	H-L41270	natural killer associated transcript 4 [NKAT4*]	50.16	65.0kDa
M306 F2	H-L41347	natural killer associated transcript 5 [NKAT5*]	33.55	40
M468 C3	H-L41351	Homo sapiens prostatic mRNA, complete cds	37.84	45.0kDa
169-53	H-L41816	Homo sapiens cam kinase I mRNA	48	40.77
167-25	H-L41939	tyrosine-protein kinase receptor EPH-3 precursor	108	108.6
C3	H-L42374	Homo sapiens protein phosphatase 2A B56-beta (PP2A) mRNA, complete cds	54.78	64
M306 B1	H-L42531	glutathione synthetase	52.25	54.0kDa
M302 F6	H-L42856	RNA polymerase II transcription factor SIII, p18 subunit	13.09	20.0kDa
M313 C7	H-L76200	guanylate kinase (GUK1)	21.78	32.0kDa
M428 E1	H-L76702	Homo sapiens protein phosphatase 2A B56-delta (PP2A) mRNA, complete cds	66.33	68.0kDa
M478 A1	H-L76703	Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds	51.48	60.0kDa
166-52	H-L77213	H.sapiens phosphomevalonate kinase mRNA	34	21.19
169-64	H-L77964	H.sapiens ERK3 mRNA	100	79.38
M360 C3	H-M10050	fatty-acid-binding protein 2, intestinal	14.08	20.0kDa
D5	H-M10050	fatty-acid-binding protein 2, intestinal	14.08	36
M421 E7	H-M10058	Asialoglycoprotein receptor 1	32.12	48.0kDa
M429 D3	H-M10901	Glucocorticoid receptor	85.58	85.0kDa
M312 G1	H-M11025	asialoglycoprotein receptor 2	34.32	34.0kDa
167-44	H-M11026	interferon alpha-4 precursor	33	20.86
F2	H-M11321	Human group-specific component vitamin D-binding protein mRNA, complete cds	52.25	56
M236 B5	H-M11354	histone H3.2, CENTRAL ROLE IN NUCLEOSOME FORMATION.	15.07	24

M236 G2	H-M11433	retinol-binding protein 1, cellular transport protein	14.96	28
M270 G7	H-M11560	aldolase A , FRUCTOSE-BISPHOSPHATE ALDOLASE A [Homo sapiens]	40.15	40
H3	H-M11717	Human heat shock protein (hsp 70) gene, complete cds	70.51	60
E1	H-M12523	Human serum albumin (ALB) gene, complete cds	67.1	70
B5	H-M12963	Alcohol dehydrogenase 1 (class I), alpha polypeptide	41.36	48
D6	H-M13228		51.15	50
D4	H-M13981	Inhibin, alpha	40.37	50
M236 G4	H-M13982	interleukin 4 [IL4] precursor, B-cell activator	16.94	30
M271 B6	H-M14043	lipocortin II, Annexin II (lipocortin II). CALCIUM-REGULATED MEMBRANE-BINDING PROTEIN	37.4	45.0kDa
M271 F4	H-M14218	argininosuccinate lyase	51.04	56
M297 A3	H-M14221	cathepsin B	37.4	32.0kDa
M305 B2	H-M14328	enolase, alpha	47.85	50
167-54	H-M14333	human c-syn protooncogene	60	59.14
167-51	H-M14505	H.sapiens mRNA (open reading frame; patient SK29(AV))	36	33.40
215-74	H-M14676	human src-like kinase (slk) mRNA	60	59.14
167-55	H-M14780	"creatine kinase, m chain"	52	41.98
M416 F8	H-M15059	Fc fragment of IgE, low affinity II, receptor for (CD23A)	35.42	45.0kDa
M271 F1	H-M15182	glucuronidase, beta [GUSB], PLAYS AN IMPORTANT ROLE IN THE DEGRADATION OF DERMATAN AND KERATAN SULFATES.	71.72	72
215-37	H-M15465	human pyruvate kinase type L mRNA	64	59.80
M298 A4	H-M15796	cyclin	28.82	43.0kDa
C3	H-M15800	Mal, T-cell differentiation protein	16.94	17
M440 E1	H-M15841	Human U2 small nuclear RNA-associated B" antigen mRNA, complete cds	24.86	34.0kDa
M248 C3	H-M15887	endozepine	9.68	15.0kDa
M463 A2	H-M15990	human c-yes-1 mRNA	59.800	65.0kDa
M418 E2	H-M16038	tyrosine-protein kinase LYN	56.390	64.0kDa
M266 D3	H-M16342	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 [Homo sapiens]; small nuclear ribonucleoprotein, polypeptide C	32.01	49
167-20	H-M16591	tyrosine-protein kinase HCK	60	55.62
C7	H-M16591	tyrosine-protein kinase HCK	55.620	70

M305 E7	H-M16660	heat shock 90kD protein 1, beta [HSPCB]	79.75	80
167-65	H-M16750	PIM-1 proto-oncogene serine/threonine-protein kinase	38	34.50
M311 A1	H-M16827	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain	46.42	50.0kDa
D3	H-M16961	Alpha-2-HS-glycoprotein alpha and beta chain	40.48	50
D3	H-M16974	Complement component 8, alpha polypeptide	64.35	55
M248 C2	H-M17017	INTERLEUKIN-8 PRECURSOR [Homo sapiens]	11	11
M305 E4	H-M17885	ribosomal phosphoprotein P0, acidic	34.98	37.0kDa
M339 E2	H-M17887	ribosomal phosphoprotein P2	12.76	19.0kDa
M248 D5	H-M18731	galactose-1-phosphate uridylyltransferase [GALT]	41.91	42
F2	H-M19309	Troponin T1, skeletal, slow	30.69	40
M385 E2	H-M19713	tropomyosin, alpha, muscle	31.35	41.0kDa
167-79	H-M19722	proto-oncogene tyrosine-protein kinase FGR	64	58.26
M248 H1	H-M20560	Annexin III (lipocortin III), INHIBITOR OF PHOSPHOLIPASE A2	35.64	37
M235 H1	H-M20681	GLUCOSE TRANSPORTER TYPE 3, BRAIN	54.67	50
167-29	H-M21616	beta platelet-derived growth factor receptor precursor	121	121.7
M305 A3	H-M21812	myosin light chain 2	18.81	30
167-30	H-M22146	"40S ribosomal protein S4, x isoform"	34	26.91
M302 D6	H-M22430	phospholipase A2 RASF-A	15.95	31.0kDa
E2	H-M22491	Bone morphogenetic protein 3 (osteogenic)	52.03	55
M340 A2	H-M22538	NADH-ubiquinone reductase, 24 kDa subunit, mitochondrial	27.5	33
B2	H-M22632	Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	47.41	47
B4	H-M22960	Protective protein for beta-galactosidase (galactosialidosis)	52.91	60
M250 C4	H-M22995	ras-related protein RAP1A, member of RAS oncogene family		
B3	H-M23254	Calpain, large polypeptide L2	77.11	77
M266 B4	H-M23613	Nucleophosmin (nucleolar phosphoprotein B23, numatrin), BELIEVED TO BIND SINGLE-STRANDED NUCLEIC ACIDS	32.45	42
M469 D2	H-M23668	Homo sapiens adrenodoxin gene	20.35	25.0kDa
M478 H3	H-M24439	Human liver/bone/kidney-type alkaline phosphatase (ALPL) gene	57.75	64.0kDa
F5	H-M24470	Glucose-6-phosphate dehydrogenase	38.06	44

M270 E5	H-M24898	thyroid hormone triiodothyronine receptor c-erbA, ear-1, Thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene homolog)	67.65	85
D3	H-M24902	Acid phosphatase, prostate	42.57	54
D6	H-M25809	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 1	56.32	57
167-77	H-M26252	"pyruvate kinase, M2 isozyme"	60	58.48
M271 F8	H-M26326	keratin 18	47.41	50.0kDa
B1	H-M26901	Human renin gene	44.44	50
M271 G4	H-M27396	asparagine synthetase	61.82	62
M338 B3	H-M27542	globulin, sex hormone-binding	39.200	40
M512 B6	H-M27602	Protease, serine, 2 (trypsin 2)	27.28	36.0kDa
M270 B6	H-M27691	DNA-binding protein CREB, cAMP-responsive	36.08	50
C1	H-M27878	Zinc finger protein 84 (HPF2)	81.29	81
M270 F6	H-M28209	guanine nucleotide-binding protein rab1	22.66	30.0kDa
M512 H5	H-M28210	RAB3A, member RAS oncogene family	24.31	36.0kDa
B3	H-M28214	Homo sapiens GTP-binding protein (RAB3B) mRNA, complete cds	24.2	34
M300 C5	H-M28249	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) [ITGA2]	130.02	130.0kDa
M248 B6	H-M28372	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) [ZNF9]	19.58	28.0kDa
M248 C5	H-M28983	interleukin 1, alpha [IL1A]	29.92	42
M298 C1	H-M29536	translation initiation factor 2, beta subunit	36.74	50.0kDa
M425 A5	H-M29696	Interleukin 7 receptor	50.6	63.0kDa
E1	H-M29960	Human steroid receptor (TR2-11) mRNA, complete cds	66.44	65
M361 D3	H-M29971	6-O-methylguanine-DNA methyltransferase [MGMT]	22.88	33.0kDa
167-67	H-M30448	"casein kinase II, beta chain"	34	23.72
M250 E2	H-M31211	MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE A ISOFORM [Homo sapiens]	22.99	30.0kDa
M311 C4	H-M31452	proline-rich protein	65.78	68
M312 H3	H-M31469	ras-like protein TC4	23.87	32.0kDa
167-41	H-M31606	"phosphorylase B kinase gamma catalytic chain, testis isoform"	50	44.7
B4	H-M31642	Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	24.09	36
M416 D8	H-M31932	Fc fragment of IgG, low affinity IIa, receptor for (CD32)	34.98	45.0kDa

M305 A8	H-M32011	neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2) [NCF2]	57.97	58
B2	H-M32315	Human tumor necrosis factor receptor mRNA, complete cds	50.82	60
M266 C2	H-M33374	cell adhesion protein SQM1	14.96	18.0kDa
M431 F1	H-M33375	dihydrodiol dehydrogenase 4	33.99	40.0kDa
G6	H-M33680	Human 26-kDa cell surface protein TAPA-1 mRNA, complete cds	26.07	24
F1	H-M33772	Human fast skeletal muscle troponin C gene	17.71	29
167-15	H-M34065	m-phase inducer phosphatase 3	55	52.10
F4	H-M34079	Human immunodeficiency virus tat transactivator binding protein-1 (tbp-1) mRNA, complete cds	44.55	52
169-86	H-M34181	"cAMP-dependent protein kinase, beta-catalytic subunit"	50	38.68
D1	H-M34379	Elastatse 2, neutrophil	29.48	35
M314 E1	H-M34671	CD59 glycoprotein precursor	14.150	20
M266 C3	H-M35252	CO-029 (GB:M35252)	26.18	30
M315 A4	H-M36035	benzodiazapine receptor (peripheral) [BZRP]	18.7	19
M300 C1	H-M36340	ADP-ribosylation factor 1	20.02	30
M312 C3	H-M36341	ADP-ribosylation factor 2	19.91	29
D6	H-M36634	Vasoactive intestinal peptide	18.81	28
169-26	H-M36881	proto-oncogene tyrosine-protein kinase LCK	60	56.06
167-76	H-M36981	nucleoside diphosphate kinase B	26	16.79
M298 D6	H-M37400	aspartate aminotransferase, cytosolic	45.54	50.0kDa
167-88	H-M37712	galactosyltransferase associated protein kinase P58/GTA	55	48.36
M424 F4	H-M38258	Retinoic acid receptor, gamma 1	50.05	58.0kDa
M266 H3	H-M38690	CD9 antigen, INVOLVED IN PLATELET ACTIVATION AND AGGREGATION.	25.19	26.0kDa
M270 A5	H-M55265	casein kinase II, alpha catalytic subunit	43.12	50
169-74	H-M55284	human protein kinase C-L (PRKCL) mRNA	80	75.09
M512 B3	H-M55514	Potassium voltage-gated channel, shaker-related subfamily, member 4	71.94	100.0kDa
M271 F5	H-M57567	ADP-ribosylation factor 5 [AR5]. INVOLVED IN PROTEIN TRAFFICKING AND ACTS AS AN ALLOSTERIC ACTIVATOR OF CHOLERA TOXIN.	19.91	32.0kDa
M250 D1	H-M57627	interleukin 10 [IL10], SUPPRESSOR FACTOR FOR TH1 IMMUNE RESPONSES (BY SIMILARITY).	19.69	27

M302 D3	H-M57730	EPH-related receptor tyrosine kinase ligand 1 precursor	22.620	36.0kDa
M248 B5	H-M58458	ribosomal protein S4, X-linked [RPS4X]	29.04	36.0kDa
M248 A5	H-M58459	ribosomal protein S4, Y-linked [RPS4Y]	29.04	36
M248 G5	H-M58525	CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM [Homo sapiens], COMT	29.92	36
M482 B2	H-M59916	Sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	69.3	69.0kDa
M390 C1	H-M60091	galactose-1-phosphate uridylyltransferase	41.8	50.0kDa
M316 B1	H-M60314	bone morphogenetic protein 5 [BMP5]	50.05	55
B4	H-M60459	Erythropoietin receptor	55.99	60
C7	H-M60483	Human protein phosphatase 2A catalytic subunit-alpha gene, complete cds	34.1	56
M462 D7	H-M60484	Human protein phosphatase 2A catalytic subunit-beta gene, complete cds	34.1	44.0kDa
A12	H-M60527	deoxycytidine kinase	28.670	50
167-5	H-M60724	human p70 ribosomal S6 kinase alpha-I mRNA	66	57.82
167-17	H-M60725	human p70 ribosomal S6 kinase alpha-II mRNA	62	55.29
M271 A4	H-M61199	cleavage signal 1, ESTs, Highly similar to CLEAVAGE SIGNAL-1 PROTEIN [Homo sapiens]	27.5	36.0kDa
B1	H-M61733	Homo sapiens erythroid membrane protein 4.1 mRNA, complete cds	70.62	71
M298 A1	H-M61764	tubulin, gamma	49.72	55.0kDa
M422 E2	H-M62505	Complement component 5 receptor 1 (C5a ligand)	38.61	38.0kDa
M313 G5	H-M62810	transcription factor 1, mitochondrial	27.17	35.0kDa
C9	H-M62839	apolipoprotein H	38.06	60
G5	H-M63154	Gastric intrinsic factor (vitamin B synthesis)	45.98	52
167-6	H-M63167	RAC-alpha serine/threonine kinase	64	52.87
B1	H-M63573	Peptidylprolyl isomerase B (cyclophilin B)	23.87	33
M302 H2	H-M63603	phospholamban	5.83	6
M306 D1	H-M63838	interferon, gamma-inducible protein 16	80.3	108
M423 H3	H-M63959	Low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1	39.38	48.0kDa

G3	H-M64099	Human gamma-glutamyl transpeptidase-related protein (GGT-Rel) mRNA, complete cds	64.57	52
M475 B8	H-M64673	Human heat shock factor 1 (TCF5) mRNA, complete cds	58.3	65.0kDa
M266 D5	H-M64716	ribosomal protein S25	13.86	17.0kDa
M248 C6	H-M64752	glutamate receptor, ionotropic, AMPA 1 [GRIA1]	99.88	100
M312 G3	H-M64925	palmitoylated membrane protein, erythrocyte, 55 kDa	51.37	51.0kDa
M302 C7	H-M65292	complement factor H-related protein (GB:M65292)	36.41	50
D3	H-M68516	Human protein C inhibitor gene, complete cds	44.77	54
167-27	H-M68520	cell division protein kinase 2	38	32.85
M236 D5	H-M68867	Cellular retinoic acid-binding protein 2, MAY REGULATE THE ACCESS OF RETINOIC ACID TO THE NUCLEAR RETINOIC ACID RECEPTORS.	15.29	19.0kDa
M441 E1	H-M69226	monoamine oxidase A [MAOA]	58.08	64.0kDa
M298 D5	H-M72393	calcium-dependent phospholipid-binding protein [PLA2*]	82.5	117.0kDa
M422 D5	H-M73238	Ciliary neurotrophic factor receptor	41.03	51.0kDa
C1	H-M73255	Human vascular cell adhesion molecule-1 (VCAM1) gene, complete CDS	81.4	81
M422 G6	H-M73481	Human gastrin releasing peptide receptor (GRPR) mRNA, complete cds	42.35	45.0kDa
M235 G6	H-M73499	carboxylesterase, INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.	62.48	90.0kDa
M302 D1	H-M73547	polyposis locus DP1	20.46	28
M300 H4	H-M73969	interleukin 8 receptor, beta [IL8RB]	39.71	36
G1	H-M74491	ADP-ribosylation factor 3	20.02	31
B4	H-M74816		49.5	50
B2	H-M75110	H,K-ATPase, beta subunit	32.12	37
M416 B8	H-M76766	General transcription factor IIB	34.87	44.0kDa
167-18	H-M77198	RAC-beta serine/threonine kinase	64	57.27
167-87	H-M77348	PMEL 17 protein precursor	74	73.55
C4	H-M77698	YY1 transcription factor	45.65	48
M248 G6	H-M80261	apurinic/aprimidinic (abasic) endonuclease [APE], REPAIRS OXIDATIVE DNA DAMAGES IN VITRO	35.09	37.0kDa
169-50	H-M80359	putative serine/threonine-protein kinase P78	80	78.50
M330 H1	H-M80461	immunoglobulin-associated beta (B29) [IGB]	25.370	27.0kDa

169-1	H-M80613	ring3 protein	100	83.01
M298 A2	H-M80783	B12 protein	34.87	43.0kDa
217-1	H-M81457	calpactin I light chain	10	10.74
M422 C6	H-M81589	Homo sapiens serotonin 1D receptor (5-HT1D') mRNA, complete cds	41.58	41.0kDa
M424 A1	H-M81590	Homo sapiens serotonin 1D receptor (5-HT1D~) mRNA, complete cds	43.01	48.0kDa
M250 H1	H-M81592	gamma-glutamyl carboxylase [GGCX], CONVERTS GLUTAMATE RESIDUES TO GAMMA-CARBOXYGLUTAMATE	83.49	85
M250 F2	H-M81601	TRANSCRIPTION ELONGATION FACTOR S-II [Homo sapiens]	33.22	36.0kDa
C2	H-M81650	Human semenogelin I (SEMGI) gene, complete cds	50.93	52
M266 A4	H-M81757	ribosomal protein S19	16.06	18
169-61	H-M81933	m-phase inducer phosphatase 1	57	57.60
M302 H1	H-M82809	annexin IV	35.42	38.0kDa
M300 C4	H-M83653	cytoplasmic phosphotyrosyl protein phosphatase, type 1	17.49	28.0kDa
169-14	H-M83941	tyrosne-protein kinase receptor ETK1 precursor	108	108.2
F1	H-M84443	Galactokinase 2	50.49	52
M305 H6	H-M84747	interleukin 9 receptor [IL9R]	57.53	58
167-53	H-M86400	14-3-3 protein zeta/delta	33	27.02
M271 C8	H-M86521	transketolase	68.64	68.0kDa
169-51	H-M86699	human kinase (TTK) mRNA	92	92.58
M316 F2	H-M86752	transformation-sensitive protein	59.84	60.0kDa
M270 C8	H-M86921	membrane glycoprotein mb-1, Immunoglobulin-associated alpha, ASSOCIATED TO SURFACE IGM-RECEPTOR; MAY BE INVOLVED IN SIGNAL TRANSDUCTION	24.97	34
A5	H-M87507	Homo sapien interleukin-1 beta convertase (IL1BCE) mRNA, complete cds	44.55	50
M305 B7	H-M88011	glucokinase [GCK]	51.26	60
M305 H1	H-M88279	immunophilin FKBP52	50.6	64.0kDa
M420 F1	H-M88468	mevalonate kinase	43.600	47.0kDa
M305 A7	H-M89913	dUTP pyrophosphatase (dUTPase) [DUT*]	15.62	19
M316 E2	H-M90657	tumor-associated antigen L6	22.33	28
167-31	H-M90813	human D-type cyclin (CCND2) mRNA	36	31.86
A1	H-M91036	H.sapiens G-gamma globin and A-gamma globin genes, complete cds's	16.28	18

G2	H-M91463	Human glucose transporter (GLUT4) gene, complete cds	55.66	52
A1	H-M91670	Human ubiquitin carrier protein (E2-EPF) mRNA, complete cds	24.86	36
E4	H-M92444	Homo sapiens apurinic/apyrimidinic endonuclease (HAP1) gene, complete cds	35.09	45
M305 C4	H-M94556	single-stranded DNA-binding protein, mitochondrial	16.39	20
G12	H-M94856	fatty-acid-binding protein homolog	14.96	36
M453 C3	H-M95623	Homo sapiens hydroxymethylbilane synthase gene, complete cds	39.82	50.0kDa
M302 F2	H-M95787	smooth muscle protein SM22	22.22	33.0kDa
A1	H-M95809	Human basic transcription factor 62kD subunit (BTF2), complete cds	60.39	64
M271 E8	H-M96982	small nuclear ribonucleoprotein U2 auxiliary factor, 35 kDa , SPLICING FACTOR U2AF 35 KD SUBUNIT. NECESSARY FOR THE SPLICING OF PRE-mRNA.	26.51	39.0kDa
M416 B3	H-M96995	Growth factor receptor-bound protein 2	23.98	32.0kDa
G2	H-M96995	Growth factor receptor-bound protein 2	23.98	49
H4	H-M97016	Bone morphogenetic protein 8 (osteogenic protein 2)	44.33	61
M271 D1	H-M97190	Sp2 transcription factor [SP2], BINDS TO GC BOX PROMOTERS ELEMENTS AND SELECTIVELY ACTIVATES mRNA SYNTHESIS FROM GENES THAT CONTAIN FUNCTIONAL RECOGNITION SITES.	54.56	60
M271 C1	H-M97191	Sp3 transcription factor [SP3], BINDS TO GT AND GC BOXES PROMOTERS ELEMENTS. PROBABLE TRANSCRIPTIONAL ACTIVATOR.	71.94	72
M305 C7	H-M97388	transcription repressor (interacting with the TATA-binding protein) [DR1*]	19.47	30
217-13	H-M97675	human transmembrane receptor (ror1) mRNA	100	103.1
B3	H-M97856	Nuclear autoantigenic sperm protein (histone-binding)	86.68	87
M429 G2	H-M97935	Homo sapiens transcription factor ISGF-3 mRNA, complete cds	82.61	89.0kDa

D1	H-M99487	Human prostate-specific membrane antigen (PSM) mRNA, complete cds	82.61	92
M363 A1	H-P0002	riboflavin synthase beta chain (ribE)	17.27	
M363 B1	H-P0004	carbonic anhydrase (icfA)	24.42	
M363 C1	H-P0005	orotidine 5'-phosphate decarboxylase (pyrF)	25.08	
M363 D1	H-P0006	pantoate-beta-alanine ligase (panC)	30.47	
M379 A1	H-P0010-2	chaperone and heat shock protein (groEL)	60.17	
M363 E1	H-P0011	co-chaperone (groES)	13.09	
M363 F1	H-P0012	DNA primase (dnaG)	61.6	
M363 G1	H-P0013	hypothetical protein	38.61	
M363 H1	H-P0014	hypothetical protein	30.36	
M363 A2	H-P0015	hypothetical protein	10.34	
M363 B2	H-P0016	hypothetical protein	9.68	
M363 C2	H-P0017	virB4 homolog (virB4)	86.68	
M363 D2	H-P0018	hypothetical protein	51.7	
M363 E2	H-P0021	hypothetical protein	21.01	
M363 F2	H-P0022	conserved hypothetical integral membrane protein	57.42	
M363 G2	H-P0026	citrate synthase (gltA)	46.97	
M363 H2	H-P0027	isocitrate dehydrogenase (icd)	46.86	
M363 A3	H-P0028	conserved hypothetical secreted protein	19.58	
M363 B3	H-P0030	hypothetical protein	65.34	
M363 C3	H-P0031	hypothetical protein	15.18	
M363 D3	H-P0034	aspartate 1-decarboxylase (panD)	12.98	
M363 E3	H-P0035	conserved hypothetical protein	10.78	
M363 F3	H-P0037	NADH-ubiquinone oxidoreductase subunit	38.72	
M363 G3	H-P0044	GDP-D-mannose dehydratase (rfbD)	42.02	
M363 H3	H-P0047	hydrogenase expression/formation protein (hypE)	36.63	
M363 A4	H-P0048	transcriptional regulator (hypF)	84.7	
M363 B4	H-P0052	hypothetical protein	36.41	
M363 C4	H-P0055	proline permease (putP)	54.67	
M363 D4	H-P0056	delta-1-pyrroline-5-carboxylate dehydrogenase	130.46	
M363 E4	H-P0057	hypothetical protein	7.7	
M363 F4	H-P0063	hypothetical protein	54.67	
M363 G4	H-P0064	hypothetical protein	15.4	
M363 H4	H-P0066	conserved hypothetical ATP-binding protein	91.52	
M363 A5	H-P0067	urease accessory protein (ureH)	29.26	
M363 B5	H-P0068	urease accessory protein (ureG)	22	
M363 C5	H-P0075	urease protein (ureC)	49.06	
M363 D5	H-P0077	peptide chain release factor RF-1 (prfA)	38.83	

M363 E5	H-P0082	methyl-accepting chemotaxis transducer (tlpC)	74.14	
M363 F5	H-P0086	conserved hypothetical protein	49.61	
M363 G5	H-P0087	hypothetical protein	50.38	
M363 H5	H-P0088	RNA polymerase sigma-70 factor (rpoD)	73.92	
M363 A6	H-P0089	pfs protein (pfs)	25.52	
M363 B6	H-P0090	malonyl coenzyme A-acyl carrier protein transacylase (fabD)	34.1	
M363 C6	H-P0093	hypothetical protein	12.21	
M363 D6	H-P0096	phosphoglycerate dehydrogenase	34.65	
M304 A1	H-P0099	methyl-accepting chemotaxis protein (tlpA)	74.36	
M304 B1	H-P0100	conserved hypothetical protein	40.59	
M304 C1	H-P0101	hypothetical protein	27.94	
M304 D1	H-P0104	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB)	64.02	
M304 E1	H-P0105	conserved hypothetical protein	17.16	
M304 F1	H-P0106	cystathionine gamma-synthase (metB)	41.91	
M304 G1	H-P0107	cysteine synthetase (cysK)	33.77	
M304 H1	H-P0108	hypothetical protein	20.57	
M304 A2	H-P0109	chaperone and heat shock protein 70 (dnaK)	68.31	
M304 B2	H-P0110	co-chaperone and heat shock protein (grpE)	20.9	
M304 C2	H-P0111	hypothetical protein	30.47	
M304 D2	H-P0113	hypothetical protein	10.89	
M304 E2	H-P0114	hypothetical protein	69.19	
M304 F2	H-P0115	flagellin B (flaB)	56.65	
M304 G2	H-P0116	DNA topoisomerase I (topA)	81.07	
M304 H2	H-P0117	conserved hypothetical protein	33.99	
M304 A3	H-P0118	hypothetical protein	43.56	
M304 B3	H-P0119	hypothetical protein	50.82	
M304 C3	H-P0120	hypothetical protein	43.89	
M304 D3	H-P0121	phosphoenolpyruvate synthase (ppsA)	89.43	
M304 E3	H-P0122	hypothetical protein	4.84	
M304 F3	H-P0123	threonyl-tRNA synthetase (thrS)	67.43	
M304 G3	H-P0124	translation initiation factor IF-3 (infC)	22.44	
M304 H3	H-P0125	ribosomal protein L35 (rpl35)	7.15	
M304 A4	H-P0126	ribosomal protein L20 (rpl20)	12.87	
M304 B4	H-P0127	outer membrane protein (omp4)	31.57	
M304 C4	H-P0128	hypothetical protein	4.62	
M304 D4	H-P0129	hypothetical protein	15.62	
M304 E4	H-P0130	hypothetical protein	31.57	
M304 F4	H-P0131	hypothetical protein	3.74	
M304 G4	H-P0132	L-serine deaminase (sdaA)	50.16	
M304 H4	H-P0133	serine transporter (sdaC)	45.54	
M304 A5	H-P0134	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase (dhs1)	49.5	
M304 B5	H-P0135	hypothetical protein	4.95	

M304 C5	H-P0136	bacterioferritin comigratory protein (bcp)	16.83	
M304 D5	H-P0137	hypothetical protein	23.32	
M304 E5	H-P0138	conserved hypothetical iron-sulfur protein	53.02	
M304 F5	H-P0139	conserved hypothetical secreted protein	26.73	
M304 G5	H-P0140	L-lactate permease (lctP)	60.5	
M304 H5	H-P0141	L-lactate permease (lctP)	60.72	
M304 A6	H-P0142	A/G-specific adenine glycosylase (mutY)	36.19	
M304 B6	H-P0144	cytochrome c oxidase, heme b and copper-binding subunit, membrane-bound (fixN)	53.79	
M304 C6	H-P0145	cytochrome c oxidase, monoheme subunit, membrane-bound (fixO)	25.63	
M304 D6	H-P0146	cbb3-type cytochrome c oxidase subunit Q (CcoQ)	8.14	
M304 E6	H-P0147	cytochrome c oxidase, diheme subunit, membrane-bound (fixP)	31.57	
M304 F6	H-P0148	hypothetical protein	7.59	
M304 G6	H-P0150	hypothetical protein	21.67	
M304 H6	H-P0152	hypothetical protein	31.68	
M304 A7	H-P0153	recombinase (recA)	38.28	
M304 B7	H-P0154	enolase (eno)	46.97	
M304 C7	H-P0155	hypothetical protein	10.12	
M304 D7	H-P0157	shikimic acid kinase I (aroK)	17.93	
M304 E7	H-P0158	hypothetical protein	35.09	
M304 F7	H-P0159	lipopolysaccharide 1,2-glucosyltransferase (rfaJ)	41.03	
M304 G7	H-P0161	hypothetical protein	4.07	
M304 H7	H-P0162	conserved hypothetical protein	26.51	
M304 A8	H-P0163	delta-aminolevulinic acid dehydratase (hemB)	35.64	
M304 B8	H-P0164	signal-transducing protein, histidine kinase	28.05	
M304 C8	H-P0165	hypothetical protein	19.14	
M304 D8	H-P0166	response regulator (ompR)	24.86	
M304 E8	H-P0167	hypothetical protein	17.38	
M304 F8	H-P0168	hypothetical protein	9.68	
M304 G8	H-P0170	hypothetical protein	27.94	
M304 H8	H-P0171	peptide chain release factor RF-2 (prfB)	40.04	
M304 A9	H-P0172	molybdopterin biosynthesis protein (moeA)	43.12	
M304 B9	H-P0173	flagellar biosynthetic protein (fliR)	28.16	
M304 C9	H-P0174	hypothetical protein	28.49	
M304 D9	H-P0175	cell binding factor 2	33	
M304 E9	H-P0176	fructose-bisphosphate aldolase (tsr)	33.88	
M304 F9	H-P0177	translation elongation factor EF-P (efp)	20.68	

M304 G9	H-P0178	spore coat polysaccharide biosynthesis protein E	37.51	
M304 H9	H-P0179	ABC transporter, ATP-binding protein	23.54	
M304 A10	H-P0180	apolipoprotein N-acyltransferase (cute)	46.86	
M304 B10	H-P0182	lysyl-tRNA synthetase (lysS)	55.22	
M304 C10	H-P0183	serine hydroxymethyltransferase (glyA)	45.87	
M304 D10	H-P0184	hypothetical protein	19.91	
M304 E10	H-P0185	hypothetical protein	29.48	
M304 F10	H-P0186	hypothetical protein	44.55	
M304 G10	H-P0187	hypothetical protein	10.56	
M304 H10	H-P0188	hypothetical protein	3.74	
M304 A11	H-P0189	conserved hypothetical integral membrane protein	19.58	
M304 B11	H-P0190	conserved hypothetical secreted protein	55.33	
M304 C11	H-P0191	fumarate reductase, iron-sulfur subunit (frdB)	27.06	
M304 D11	H-P0192	fumarate reductase, flavoprotein subunit (frdA)	78.65	
M304 E11	H-P0193	fumarate reductase, cytochrome b subunit (frdC)	28.16	
M304 F11	H-P0194	triosephosphate isomerase (tpi)	25.85	
M304 G11	H-P0195	enoyl-(acyl-carrier-protein) reductase (NADH) (fabI)	30.36	
M365 A1	H-P0197	S-adenosylmethionine synthetase 2 (metX)	42.46	
M365 B1	H-P0203	hypothetical protein	10.12	
M365 C1	H-P0209	hypothetical protein	49.61	
M365 D1	H-P0213	glucose inhibited division protein (gidA)	68.42	
M381 E1	H-P0218	hypothetical protein	20.24	
M365 E1	H-P0221	nifU-like protein	35.97	
M365 F1	H-P0227	outer membrane protein (omp5)	76.12	
M365 G1	H-P0228	conserved hypothetical integral membrane protein	43.01	
M365 H1	H-P0230	CTP: CMP-3-deoxy-D-manno-octulosonate-cytidylyl-transferase (kdsB)	26.84	
M365 A2	H-P0233	conserved hypothetical protein	43.01	
M365 B2	H-P0235	conserved hypothetical secreted protein	39.16	
M365 C2	H-P0236	hypothetical protein	13.64	
M365 D2	H-P0238	prolyl-tRNA synthetase (proS)	63.58	
M381 E2	H-P0243	neutrophil activating protein (napA) (bacterioferritin)	15.95	
M365 E2	H-P0244	signal-transducing protein, histidine kinase (atoS)	42.02	
M365 F2	H-P0246	flagellar basal-body P-ring protein (flgI)	37.73	

M365 G2	H-P0247	ATP-dependent RNA helicase, DEAD-box family (deaD)	54.23	
M365 H2	H-P0248	conserved hypothetical protein	39.93	
M379 B1	H-P0249-2	hypothetical protein	19.8	
M379 C1	H-P0250-2	oligopeptide ABC transporter, ATP-binding protein (oppD)	56.87	
M381 A3	H-P0251	oligopeptide ABC transporter, permease protein (oppC)	37.29	
M379 E1	H-P0252-2	outer membrane protein (omp7)	53.68	
M365 A3	H-P0254	outer membrane protein (omp8)	47.52	
M365 B3	H-P0255	adenylosuccinate synthetase (purA)	45.32	
M365 C3	H-P0257	conserved hypothetical secreted protein	24.2	
M365 D3	H-P0259	exonuclease VII, large subunit (xseA)	46.31	
M381 D3	H-P0260	adenine specific DNA methyltransferase (mod)	42.35	
M365 E3	H-P0263	adenine specific DNA methyltransferase (hpaim)	27.83	
M365 F3	H-P0264	ATP-dependent protease binding subunit (clpB)	94.27	
M365 G3	H-P0266	dihydroorotase (pyrC)	41.69	
M365 H3	H-P0267	chlorohydrolase	45.1	
M365 A4	H-P0271	hypothetical protein	36.08	
M365 B4	H-P0275	ATP-dependent nuclease (addB)	47.41	
M381 G3	H-P0276	hypothetical protein	20.46	
M365 C4	H-P0278	guanosine pentaphosphate phosphohydrolase (gppA)	53.35	
M365 D4	H-P0279	lipopolysaccharide heptosyltransferase-1 (rfaC)	37.51	
M365 E4	H-P0280	heat shock protein B (ibpB)	36.19	
M365 F4	H-P0282	hypothetical protein	52.91	
M365 G4	H-P0283	3-dehydroquinate synthase (aroB)	37.84	
M365 H4	H-P0284	conserved hypothetical integral membrane protein	57.64	
M365 A5	H-P0285	conserved hypothetical protein	46.09	
M381 A4	H-P0287	hypothetical protein	19.03	
M381 C4	H-P0288	hypothetical protein	17.38	
M366 A1	H-P0389	superoxide dismutase (sodB)	23.54	
M366 B1	H-P0390	adhesin-thiol peroxidase (tagD)	18.37	
M366 C1	H-P0391	purine-binding chemotaxis protein (cheW)	18.26	
M366 D1	H-P0392	histidine kinase (cheA)	88.44	
M366 E1	H-P0393	chemotaxis protein (cheV)	34.32	
M366 F1	H-P0394	hypothetical protein	27.83	
M366 G1	H-P0395	conserved hypothetical protein	24.53	
M366 H1	H-P0396	conserved hypothetical protein	67.87	
M366 A2	H-P0397	phosphoglycerate dehydrogenase (serA)	57.75	
M366 B2	H-P0398	hypothetical protein	20.13	
M366 C2	H-P0399	ribosomal protein S1 (rps1)	61.27	

M366 D2	H-P0403	phenylalanyl-tRNA synthetase, alpha subunit (pheS)	36.19	
M366 E2	H-P0404	protein kinase C inhibitor (SP:P16436)	11.55	
M366 F2	H-P0405	nifS-like protein	48.51	
M366 G2	H-P0406	hypothetical protein	21.67	
M366 H2	H-P0407	biotin sulfoxide reductase (bisC)	87.67	
M381 D1	H-P0409	GMP synthase (guaA)	55.99	
M381 F1	H-P0410	putative neuraminylactose-binding hemagglutinin homolog (hpaA)	27.5	
M366 A3	H-P0411	hypothetical protein	11.66	
M366 B3	H-P0412	hypothetical protein	3.63	
M366 C3	H-P0413	transposase-like protein, PS3IS	29.59	
M366 D3	H-P0414	IS200 insertion sequence from SARA17	15.29	
M366 E3	H-P0415	conserved hypothetical integral membrane protein	68.64	
M366 F3	H-P0416	cyclopropane fatty acid synthase (cfa)	42.9	
M366 G3	H-P0417	methionyl-tRNA synthetase (metS)	71.61	
M366 H3	H-P0418	hypothetical protein	36.96	
M366 A4	H-P0419	conserved hypothetical protein	28.82	
M366 B4	H-P0420	hypothetical protein	15.73	
M366 C4	H-P0421	type 1 capsular polysaccharide biosynthesis protein J (capJ)	42.9	
M366 D4	H-P0422	arginine decarboxylase (speA)	67.76	
M366 E4	H-P0424	hypothetical protein	68.2	
M366 F4	H-P0425	hypothetical protein	45.98	
M366 G4	H-P0427	hypothetical protein	12.32	
M366 H4	H-P0433	hypothetical protein	16.28	
M366 A5	H-P0436	hypothetical protein	13.42	
M366 B5	H-P0437	IS605 transposase (tmpA)	15.73	
M366 C5	H-P0438	IS605 transposase (tmpB)	47.08	
M366 D5	H-P0442	hypothetical protein	9.79	
M366 E5	H-P0445	hypothetical protein	6.82	
M366 F5	H-P0452	hypothetical protein	57.09	
M366 G5	H-P0455	hypothetical protein	11.44	
M366 H5	H-P0457	hypothetical protein	9.68	
M366 A6	H-P0463	type I restriction enzyme M protein (hsdM)	53.68	
M366 B6	H-P0464	type I restriction enzyme R protein (hsdR)	116.16	
M366 C6	H-P0465	conserved hypothetical protein	69.52	
M366 D6	H-P0466	conserved hypothetical protein	28.16	
M366 E6	H-P0467	conserved hypothetical integral membrane protein	12.76	
M366 F6	H-P0468	conserved hypothetical protein	54.56	
M366 G6	H-P0469	conserved hypothetical protein	17.93	
M366 H6	H-P0471	glutathione-regulated potassium-efflux system protein (kefB)	45.87	
M366 A7	H-P0472	outer membrane protein (omp11)	20.57	

M366 B7	H-P0473	molybdenum ABC transporter, periplasmic molybdate-binding protein (modA)	27.17	
M366 C7	H-P0474	molybdenum ABC transporter, permease protein (modB)	24.75	
M366 D7	H-P0475	molybdenum ABC transporter, ATP-binding protein (modD)	29.26	
M366 E7	H-P0476	glutamyl-tRNA synthetase (gltX)	51.04	
M366 F7	H-P0477	outer membrane protein (omp12)	40.48	
M366 G7	H-P0478	adenine specific DNA methyltransferase (VSPIM)	60.06	
M366 H7	H-P0479	hypothetical protein	31.13	
M366 A8	H-P0481	adenine specific DNA methyltransferase (MFOKI)	23.32	
M366 B8	H-P0482	hypothetical protein	18.81	
M366 C8	H-P0483	cytosine specific DNA methyltransferase (H-PHMC)	36.3	
M367 A1	H-P0486	hypothetical protein	58.19	
M367 B1	H-P0487	hypothetical protein	52.91	
M367 C1	H-P0489	hypothetical protein	32.56	
M367 D1	H-P0490	putative potassium channel protein, putative	41.69	
M367 E1	H-P0491	ribosomal protein L28 (rpl28)	6.93	
M367 F1	H-P0492	hypothetical protein	30.69	
M367 G1	H-P0494	UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD)	46.53	
M367 H1	H-P0495	hypothetical protein	9.57	
M367 A2	H-P0496	conserved hypothetical protein	14.74	
M367 B2	H-P0498	sodium- and chloride-dependent transporter	48.73	
M367 C2	H-P0499	phospholipase A1 precursor (DR-phospholipase A)	39.16	
M367 D2	H-P0500	DNA polymerase III beta-subunit (dnaN)	41.25	
M367 E2	H-P0501	DNA gyrase, sub B (gyrB)	85.14	
M367 F2	H-P0503	hypothetical protein	27.17	
M367 G2	H-P0504	hypothetical protein	5.5	
M367 H2	H-P0505	hypothetical protein	17.05	
M367 A3	H-P0507	conserved hypothetical protein	23.43	
M367 B3	H-P0509	glycolate oxidase subunit (gldD)	50.6	
M367 C3	H-P0510	dihydrodipicolinate reductase (dapB)	28.05	
M367 D3	H-P0512	glutamine synthetase (glnA)	53.02	
M367 E3	H-P0514	ribosomal protein L9 (rpl9)	16.61	
M367 F3	H-P0515	heat shock protein (hslV)	19.91	
M367 G3	H-P0516	heat shock protein (hslU) ORF1	48.84	
M367 H3	H-P0517	GTP-binding protein (era)	33.33	
M367 A4	H-P0519	conserved hypothetical protein	30.47	
M367 B4	H-P0520	cag pathogenicity island protein (cag1)	12.76	
M367 C4	H-P0522	cag pathogenicity island protein (cag3)	53.02	

M367 D4	H-P0523	cag pathogenicity island protein (cag4)	18.7	
M367 E4	H-P0525	virB11 homolog	36.41	
M367 F4	H-P0526	cag pathogenicity island protein (cag6)	22	
M367 G4	H-P0528	cag pathogenicity island protein (cag8)	57.53	
M379 H1	H-P0531-2	cag pathogenicity island protein (cag11)	24.09	
M367 H4	H-P0532	cag pathogenicity island protein (cag12)	30.91	
M367 A5	H-P0534	cag pathogenicity island protein (cag13)	21.67	
M367 B5	H-P0541	cag pathogenicity island protein (cag20)	40.81	
M367 C5	H-P0542	cag pathogenicity island protein (cag21)	15.73	
M367 D5	H-P0545	cag pathogenicity island protein (cag24)	22.88	
M367 E5	H-P0549	glutamate racemase (glr)	28.16	
M367 F5	H-P0550	transcription termination factor Rho (rho)	48.29	
M367 G5	H-P0551	ribosomal protein L31 (rpl31)	7.48	
M367 H5	H-P0552	conserved hypothetical protein	31.68	
M367 A6	H-P0553	conserved hypothetical protein	25.08	
M367 B6	H-P0554	hypothetical protein	35.42	
M367 C6	H-P0555	hypothetical protein	30.14	
M367 D6	H-P0556	hypothetical protein	16.06	
M367 E6	H-P0557	acetyl-coenzyme A carboxylase (accA)	34.43	
M367 F6	H-P0558	beta ketoacyl-acyl carrier protein synthase II (fabF)	45.43	
M367 G6	H-P0561	3-ketoacyl-acyl carrier protein reductase (fabG)	27.28	
M367 H6	H-P0562	ribosomal protein S21 (rps21)	7.81	
M367 A7	H-P0563	hypothetical protein	45.87	
M367 B7	H-P0566	diaminopimelate epimerase (dapF)	30.14	
M367 C7	H-P0568	hypothetical protein	28.16	
M367 D7	H-P0570	aminopeptidase a/i (pepA)	54.67	
M367 E7	H-P0571	conserved hypothetical integral membrane protein	21.23	
M379 A2	H-P0572-2	adenine phosphoribosyltransferase (apt)	19.8	
M379 B2	H-P0573-2	hypothetical protein	12.21	
M379 C2	H-P0574-2	galactosidase acetyltransferase (lacA)	16.72	
M379 D2	H-P0575-2	conserved hypothetical membrane protein	25.63	
M379 E2	H-P0576-2	signal peptidase I (lepB)	32.01	
M367 F7	H-P0577	methylene-tetrahydrofolate dehydrogenase (folD)	32.23	
M367 G7	H-P0579	hypothetical protein	20.35	

M367 H7	H-P0580	hypothetical protein	41.03	
M367 A8	H-P0581	dihydroorotase (pyrC)	37.4	
M367 B8	H-P0582	hypothetical protein	35.75	
M367 C8	H-P0583	hypothetical protein	32.34	
M368 A1	H-P0584	flagellar switch protein (fliN)	13.64	
M368 B1	H-P0585	endonuclease III (nth)	24.09	
M368 C1	H-P0587	aminodeoxychorismate lyase (pabC)	36.3	
M368 D1	H-P0591	ferredoxin oxidoreductase, gamma subunit	20.57	
M368 E1	H-P0593	adenine specific DNA methyltransferase (mod)	65.89	
M368 F1	H-P0594	hypothetical protein	6.05	
M368 G1	H-P0596	hypothetical protein	21.23	
M368 H1	H-P0597	penicillin-binding protein 1A (PBP-1A)	72.6	
M368 A2	H-P0599	hemolysin secretion protein precursor (hylB)	47.74	
M368 B2	H-P0601	flagellin A (flaA)	56.21	
M368 C2	H-P0602	endonuclease III	24.09	
M368 D2	H-P0603	hypothetical protein	20.9	
M379 F2	H-P0608-2	hypothetical protein	17.71	
M368 E2	H-P0614	hypothetical protein	12.32	
M368 F2	H-P0616	chemotaxis protein (cheV)	34.54	
M368 G2	H-P0617	aspartyl-tRNA synthetase (aspS)	63.58	
M368 H2	H-P0621	DNA mismatch repair protein (MutS)	83.93	
M368 A3	H-P0622	hypothetical protein	13.31	
M368 B3	H-P0623	UDP-N-acetylmuramate-alanine ligase (murC)	49.5	
M368 C3	H-P0625	protein E (gcpE)	39.6	
M368 D3	H-P0626	tetrahydrodipicolinate N-succinyltransferase (dapD)	44.22	
M368 E3	H-P0627	hypothetical protein	12.21	
M368 F3	H-P0629	hypothetical protein	75.02	
M368 G3	H-P0630	modulator of drug activity (mda66)	21.45	
M368 H3	H-P0631	quinone-reactive Ni/Fe hydrogenase, small subunit (hydA)	42.35	
M368 A4	H-P0632	quinone-reactive Ni/Fe hydrogenase, large subunit (hydB)	63.69	
M368 B4	H-P0633	quinone-reactive Ni/Fe hydrogenase, cytochrome b subunit (hydC)	24.75	
M368 C4	H-P0634	quinone-reactive Ni/Fe hydrogenase (hydD)	19.69	
M368 D4	H-P0635	hypothetical protein	56.43	
M368 E4	H-P0636	hypothetical protein	10.23	
M368 F4	H-P0637	hypothetical protein	16.61	
M368 G4	H-P0638	outer membrane protein (omp13)	33.66	
M368 H4	H-P0643	glutamyl-tRNA synthetase (gltX)	48.4	

M368 A5	H-P0644	conserved hypothetical integral membrane protein	10.78	
M368 B5	H-P0645	soluble lytic murein transglycosylase (slt)	61.71	
M368 C5	H-P0646	UDP-glucose pyrophosphorylase (galU)	30.14	
M368 D5	H-P0647	hypothetical protein	14.96	
M368 E5	H-P0648	UDP-N-acetylglucosamine enolpyruvyl transferase (murZ)	46.53	
M368 F5	H-P0649	aspartate ammonia-lyase (aspA)	51.59	
M368 G5	H-P0650	hypothetical protein	21.67	
M379 A3	H-P0651-2	fucosyltransferase	52.47	
M381 E3	H-P0652	phosphoserine phosphatase (serB)	22.88	
M368 H5	H-P0653	nonheme iron-containing ferritin (pfr)	18.48	
M379 G2	H-P0654-2	conserved hypothetical protein	39.71	
M379 H2	H-P0655-2	protective surface antigen D15	100.87	
M368 A6	H-P0656	conserved hypothetical protein	42.24	
M368 B6	H-P0657	processing protease (ymxG)	47.63	
M368 C6	H-P0658	PET112-like protein	52.36	
M368 D6	H-P0659	hypothetical protein	45.65	
M368 E6	H-P0660	hypothetical protein	37.29	
M368 F6	H-P0661	ribonuclease H (rnhA)	15.84	
M368 G6	H-P0662	ribonuclease III (rnc)	26.51	
M368 H6	H-P0663	chorismate synthase (aroC)	40.26	
M368 A7	H-P0665	oxygen-independent coproporphyrinogen III oxidase (hemN)	50.38	
M368 B7	H-P0667	hypothetical protein	9.46	
M368 C7	H-P0668	hypothetical protein	66.88	
M368 D7	H-P0671	outer membrane protein (omp14)	29.81	
M368 E7	H-P0672	solute-binding signature and mitochondrial signature protein (aspB)	43.01	
M379 B3	H-P0673-2	hypothetical protein	46.97	
M381 H3	H-P0674	hypothetical protein	25.19	
M368 F7	H-P0676	methylated-DNA--protein-cysteine methyltransferase (dat1)	18.59	
M368 G7	H-P0677	conserved hypothetical integral membrane protein	28.16	
M368 H7	H-P0679	lipopolysaccharide biosynthesis protein (wbpB)	31.9	
M369 A1	H-P0681	hypothetical protein	18.59	
M369 B1	H-P0682	hypothetical protein	13.97	
M369 C1	H-P0683	UDP-N-acetylglucosamine pyrophosphorylase (glmU)	47.74	
M369 D1	H-P0685	flagellar biosynthetic protein (fliP)	19.03	
M369 E1	H-P0687	iron(II) transport protein (feoB)	70.73	
M369 F1	H-P0688	hypothetical protein	18.37	
M369 G1	H-P0690	acetyl coenzyme A acetyltransferase (thiolase) (fadA)	43.12	

M381 A1	H-P0691	3-oxoadipate coA-transferase subunit A (yxjD)	25.63	
M381 B1	H-P0692	3-oxoadipate coA-transferase subunit B (yxjE)	22.88	
M369 H1	H-P0694	hypothetical protein	28.38	
M369 A2	H-P0695	hydantoin utilization protein A (hyuA)	78.54	
M369 B2	H-P0697	hypothetical protein	18.59	
M369 C2	H-P0699	hypothetical protein	37.73	
M369 D2	H-P0700	diacylglycerol kinase (dgkA)	14.19	
M369 E2	H-P0701	DNA gyrase, sub A (gyrA)	91.08	
M369 F2	H-P0703	response regulator	42.02	
M369 G2	H-P0707	conserved hypothetical protein	33.99	
M369 H2	H-P0711	hypothetical protein	44.77	
M369 A3	H-P0715	ABC transporter, ATP-binding protein	26.51	
M369 B3	H-P0716	conserved hypothetical protein	14.74	
M369 C3	H-P0718	conserved hypothetical integral membrane protein	23.21	
M369 D3	H-P0719	hypothetical protein	12.1	
M369 E3	H-P0723	L-asparaginase II (ansB)	36.41	
M369 F3	H-P0724	anaerobic C4-dicarboxylate transport protein (dcuA)	48.84	
M369 G3	H-P0727	transcriptional regulator, putative	36.19	
M369 H3	H-P0728	conserved hypothetical protein	37.07	
M369 A4	H-P0730	hypothetical protein	11.22	
M369 B4	H-P0732	hypothetical protein	13.09	
M369 C4	H-P0734	conserved hypothetical protein	48.4	
M369 D4	H-P0735	xanthine guanine phosphoribosyl transferase (gpt)	16.94	
M369 E4	H-P0737	conserved hypothetical integral membrane protein	17.49	
M381 H2	H-P0738	D-alanine:D-alanine ligase A (ddlA)	38.28	
M369 F4	H-P0739	2-hydroxy-6-oxohepta-2,4-dienoate hydrolase	26.62	
M369 G4	H-P0741	conserved hypothetical protein	17.82	
M369 H4	H-P0745	conserved hypothetical protein	36.08	
M369 A5	H-P0747	conserved hypothetical protein	43.34	
M369 B5	H-P0748	cell division protein (ftsE)	24.64	
M369 C5	H-P0749	cell division membrane protein (ftsX)	29.59	
M369 D5	H-P0750	hypothetical protein	44.11	
M369 E5	H-P0752	flagellar hook-associated protein 2 (fliD)	74.25	
M381 F3	H-P0755	molybdopterin biosynthesis protein (moeB)	23.21	
M379 C3	H-P0757-2	beta-alanine synthetase homolog	32.23	
M369 F5	H-P0758	conserved hypothetical integral membrane protein	48.18	
M369 G5	H-P0759	conserved hypothetical integral membrane protein	45.98	
M369 H5	H-P0761	hypothetical protein	22.11	

M369 A6	H-P0762	hypothetical protein	20.46	
M369 B6	H-P0767	hypothetical protein	2.75	
M369 C6	H-P0768	molybdenum cofactor biosynthesis protein A (moaA)	35.42	
M369 D6	H-P0769	molybdopterin-guanine dinucleotide biosynthesis protein A (mobA)	22.22	
M369 E6	H-P0771	hypothetical protein	27.06	
M369 F6	H-P0772	N-acetylmuramoyl-L-alanine amidase (amiA)	48.51	
M369 G6	H-P0773	hypothetical protein	40.04	
M369 H6	H-P0777	uridine 5'-monophosphate (UMP) kinase (pyrH)	26.51	
M370 A1	H-P0782	hypothetical protein	50.16	
M370 B1	H-P0783	hypothetical protein	18.26	
M370 C1	H-P0792	sigma-54 interacting protein	55.77	
M370 D1	H-P0793	polypeptide deformylase (def)	19.25	
M370 E1	H-P0794	ATP-dependent clp protease proteolytic component (clpP)	21.67	
M370 F1	H-P0796	outer membrane protein (omp18)	30.69	
M379 G3	H-P0797-2	flagellar sheath adhesin hpaA	28.71	
M379 H3	H-P0798-2	molybdenum cofactor biosynthesis protein C (moaC)	17.49	
M370 G1	H-P0799	molybdopterin biosynthesis protein (mog)	19.47	
M370 H1	H-P0800	molybdopterin converting factor, subunit 2 (moaE)	16.06	
M379 A4	H-P0801-2	molybdopterin converting factor, subunit 1 (moaD)	8.25	
M379 B4	H-P0802-2	GTP cyclohydrolase II (ribA)	21.23	
M379 D3	H-P0803-2	hypothetical protein	30.8	
M379 E3	H-P0804-2	GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase (ribA, ribB)	37.95	
M379 F3	H-P0805-2	lipooligosaccharide 5G8 epitope biosynthesis-associated protein (lex2B)	31.35	
M370 A2	H-P0806	hypothetical protein	22.77	
M379 C4	H-P0807-2	iron(III) dicitrate transport protein (fecA)	86.68	
M370 B2	H-P0808	holo-acyl synthase (acpS)	13.2	
M370 C2	H-P0809	hypothetical protein	20.24	
M370 D2	H-P0810	conserved hypothetical protein	22.11	
M370 E2	H-P0811	hypothetical protein	11.99	
M370 F2	H-P0812	hypothetical protein	37.07	
M370 G2	H-P0813	conserved hypothetical protein	22.66	
M370 H2	H-P0814	thiamin biosynthesis protein (thiF)	28.16	
M370 A3	H-P0815	flagellar motor rotation protein (motA)	28.38	
M370 B3	H-P0831	conserved hypothetical ATP binding protein	21.67	
M379 D4	H-P0832-2	spermidine synthase (speE)	28.93	

M379 E4	H-P0833-2	hypothetical protein	32.23	
M370 C3	H-P0834	GTP-binding protein homologue (yphC)	50.49	
M370 D3	H-P0835	histone-like DNA-binding protein HU (hup)	10.45	
M370 E3	H-P0836	hypothetical protein	13.2	
M370 F3	H-P0837	hypothetical protein	11.33	
M370 G3	H-P0838	hypothetical protein	22.66	
M370 H3	H-P0839	outer membrane protein P1 (ompP1)	64.68	
M370 A4	H-P0840	flaA1 protein	36.74	
M370 B4	H-P0841	pantothenate metabolism flavoprotein (dfp)	46.86	
M370 C4	H-P0843	thiamin phosphate pyrophosphorylase/hydroxyethylthiazole kinase (thiB)	24.2	
M370 D4	H-P0845	thiamin phosphate pyrophosphorylase/hydroxyethylthiazole kinase (thiM)	30.14	
M370 E4	H-P0850	type I restriction enzyme M protein (hsdM)	58.08	
M370 F4	H-P0851	conserved hypothetical integral membrane protein	25.08	
M370 G4	H-P0854	GMP reductase (guaC)	36.08	
M370 H4	H-P0858	ADP-heptose synthase (rfaE)	50.82	
M370 A5	H-P0859	ADP-L-glycero-D-mannoheptose-6-epimerase (rfaD)	36.41	
M370 B5	H-P0861	hypothetical protein	27.17	
M370 C5	H-P0862	hypothetical protein	24.64	
M379 F4	H-P0863-2	hypothetical protein	59.73	
M370 D5	H-P0865	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)	16.06	
M370 E5	H-P0866	transcription elongation factor GreA (greA)	18.15	
M379 G4	H-P0867-2	lipid A disaccharide synthetase (lpxB)	39.71	
M379 H4	H-P0870-2	flagellar hook (flgE)	79.09	
M370 F5	H-P0871	CDP-diglyceride hydrolase (cdh)	26.95	
M370 G5	H-P0872	alkylphosphonate uptake protein (phnA)	12.1	
M370 H5	H-P0873	hypothetical protein	7.92	
M371 A1	H-P0879	hypothetical protein	22.33	
M371 B1	H-P0883	Holliday junction DNA helicase (ruvA)	20.24	
M371 C1	H-P0885	virulence factor mviN protein (mviN)	50.82	
M371 D1	H-P0886	cysteinyI-tRNA synthetase (cysS)	51.26	
M371 E1	H-P0889	iron(III) dicitrate ABC transporter, permease protein (fecD)	35.97	
M371 F1	H-P0890	conserved hypothetical protein	28.27	
M371 G1	H-P0891	conserved hypothetical protein	19.25	
M371 H1	H-P0892	conserved hypothetical protein	10.01	

M371 A2	H-P0894	conserved hypothetical protein	9.79	
M371 B2	H-P0895	hypothetical protein	13.86	
M371 C2	H-P0896	outer membrane protein (omp19)	77.99	
M371 D2	H-P0897	hypothetical protein	22.99	
M371 E2	H-P0898	hydrogenase expression/formation protein (hypD)	40.81	
M371 F2	H-P0899	hydrogenase expression/formation protein (hypC)	8.58	
M371 G2	H-P0900	hydrogenase expression/formation protein (hypB)	26.73	
M371 H2	H-P0905	phosphotransacetylase (pta)	24.64	
M371 A3	H-P0906	hypothetical protein	58.08	
M371 B3	H-P0907	hook assembly protein, flagella (flgD)	33.22	
M371 C3	H-P0909	hypothetical protein	22.22	
M371 D3	H-P0912	outer membrane protein (omp20)	56.76	
M371 E3	H-P0913	outer membrane protein (omp21)	58.3	
M371 F3	H-P0914	hypothetical protein	56.65	
M371 G3	H-P0915	iron-regulated outer membrane protein (frpB)	61.93	
M371 H3	H-P0916	iron-regulated outer membrane protein (frpB)	27.5	
M380 A1	H-P0917-2	hypothetical protein	2.64	
M371 A4	H-P0918	hypothetical protein	15.84	
M371 B4	H-P0920	conserved hypothetical integral membrane protein	25.41	
M371 C4	H-P0921	glyceraldehyde-3-phosphate dehydrogenase (gap)	36.63	
M371 D4	H-P0923	outer membrane protein (omp22)	40.7	
M371 E4	H-P0925	recombinational DNA repair protein (recR)	21.34	
M371 F4	H-P0927	heat shock protein (htpX)	35.97	
M371 G4	H-P0928	GTP cyclohydrolase I (folE)	19.91	
M371 H4	H-P0929	geranyltranstransferase (ispA)	33.44	
M371 A5	H-P0930	stationary-phase survival protein (surE)	29.48	
M371 B5	H-P0931	hypothetical protein	16.17	
M371 C5	H-P0932	hypothetical protein	11.11	
M371 D5	H-P0933	hypothetical protein	22.11	
M371 E5	H-P0934	conserved hypothetical protein	27.72	
M371 F5	H-P0935	hypothetical protein	17.82	
M371 G5	H-P0936	proline/betaine transporter (proP)	42.9	
M371 H5	H-P0938	hypothetical protein	12.76	
M371 A6	H-P0939	amino acid ABC transporter, permease protein (yckJ)	26.18	
M371 B6	H-P0940	amino acid ABC transporter, periplasmic binding protein (yckK)	28.27	
M371 C6	H-P0941	alanine racemase, biosynthetic (alr)	41.58	
M371 D6	H-P0942	D-alanine glycine permease (dagA)	49.61	

M371 E6	H-P0943	D-amino acid dehydrogenase (dadA)	45.21	
M371 F6	H-P0944	translation initiation inhibitor, putative	13.86	
M371 G6	H-P0946	conserved hypothetical integral membrane protein	54.67	
M371 H6	H-P0947	hypothetical protein	13.31	
M371 A7	H-P0949	conserved hypothetical secreted protein	16.61	
M371 B7	H-P0950	acetyl-CoA carboxylase beta subunit (accD)	31.9	
M371 C7	H-P0951	hypothetical protein	22.66	
M371 D7	H-P0952	conserved hypothetical integral membrane protein	24.09	
M371 E7	H-P0953	hypothetical protein	20.79	
M371 F7	H-P0955	prolipoprotein diacylglycerol transferase (lgt)	31.35	
M371 G7	H-P0956	conserved hypothetical protein	26.73	
M371 H7	H-P0957	3-deoxy-d-manno-octulosonic-acid transferase (kdtA)	43.34	
M371 A8	H-P0958	hypothetical protein	28.05	
M371 B8	H-P0960	glycyl-tRNA synthetase, alpha subunit (glyQ)	33.44	
M371 C8	H-P0961	glycerol-3-phosphate dehydrogenase (NAD(P)+)	34.43	
M380 B1	H-P0965-2	hypothetical protein	48.84	
M371 D8	H-P0966	conserved hypothetical protein	60.5	
M380 F1	H-P0968-2	hypothetical protein	2.42	
M371 E8	H-P0969	cation efflux system protein (czcA)	112.31	
M371 F8	H-P0970	nickel-cobalt-cadmium resistance protein (nccB)	39.6	
M371 G8	H-P0971	hypothetical protein	45.54	
M371 H8	H-P0972	glycyl-tRNA synthetase, beta subunit (glyS)	77.22	
M371 A9	H-P0973	hypothetical protein	38.94	
M380 C1	H-P0974-2	phosphoglycerate mutase (pgm)	54.12	
M380 D1	H-P0975-2	conserved hypothetical protein	10.34	
M380 E1	H-P0976-2	adenosylmethionine-8-amino-7-oxononanoate aminotransferase (bioA)	48.07	
M380 H1	H-P0994-2	hypothetical protein	29.48	
M380 G1	H-P1000-2	PARA protein	24.09	
M380 A2	H-P1001-2	hypothetical protein	10.45	
M380 B2	H-P1002-2	hypothetical protein	43.45	
M380 C2	H-P1003-2	hypothetical protein	40.81	
M380 D2	H-P1004-2	hypothetical protein	30.14	
M380 E2	H-P1005-2	hypothetical protein	11.55	
M380 F2	H-P1006-2	conjugal transfer protein (traG)	19.58	
M380 G2	H-P1017-2	amino acid permease (rocE)	57.2	
M380 H2	H-P1042-2	hypothetical protein	38.39	
M380 A3	H-P1056-2	hypothetical protein	31.35	

M380 B3	H-P1075-2	conserved hypothetical secreted protein	48.29	
M373 A1	H-P1076	hypothetical protein	18.92	
M373 B1	H-P1077	nickel transport protein (nixA)	36.52	
M373 C1	H-P1080	conserved hypothetical integral membrane protein	20.9	
M373 D1	H-P1081	hypothetical protein	22.88	
M373 E1	H-P1082	multidrug resistance protein (msbA)	60.72	
M373 F1	H-P1083	hypothetical protein	52.8	
M373 G1	H-P1084	aspartate transcarbamoylase (pyrB)	33.88	
M373 H1	H-P1085	hypothetical protein	18.92	
M373 A2	H-P1086	hemolysin (tly)	25.96	
M373 B2	H-P1087	riboflavin biosynthesis regulatory protein (ribC)	30.91	
M373 C2	H-P1088	transketolase A (tktA)	70.62	
M373 D2	H-P1091	alpha-ketoglutarate permease (kgtP)	46.97	
M373 E2	H-P1092	flagellar basal-body rod protein (flgG)	29.7	
M373 F2	H-P1096	IS605 transposase (tnpA)	15.73	
M373 G2	H-P1098	conserved hypothetical secreted protein	32.01	
M373 H2	H-P1101	glucose-6-phosphate dehydrogenase (g6pD)	46.86	
M373 A3	H-P1102	glucose-6-phosphate 1-dehydrogenase (devB)	25.08	
M373 B3	H-P1103	glucokinase (glk)	37.07	
M373 C3	H-P1108	pyruvate ferredoxin oxidoreductase, gamma subunit	20.57	
M373 D3	H-P1109	pyruvate ferredoxin oxidoreductase, delta subunit	14.41	
M373 E3	H-P1110	pyruvate ferredoxin oxidoreductase, alpha subunit	44.88	
M373 F3	H-P1111	pyruvate ferredoxin oxidoreductase, beta subunit	34.65	
M373 G3	H-P1112	adenylosuccinate lyase (purB)	48.51	
M380 C3	H-P1113-2	outer membrane protein (omp24)	30.58	
M373 H3	H-P1117	conserved hypothetical secreted protein	28.27	
M373 A4	H-P1120	hypothetical protein	15.95	
M373 B4	H-P1121	cytosine specific DNA methyltransferase (BSP6IM)	34.43	
M380 D3	H-P1122-2	hypothetical protein	8.47	
M373 C4	H-P1123	peptidyl-prolyl cis-trans isomerase, FKBP-type rotamase (slyD)	20.46	
M373 D4	H-P1124	hypothetical protein	36.52	
M373 E4	H-P1125	peptidoglycan associated lipoprotein precursor (omp18)	19.8	
M373 F4	H-P1126	colicin tolerance-like protein (tolB)	45.98	

M373 G4	H-P1128	hypothetical protein	9.35	
M373 H4	H-P1129	biopolymer transport protein (exbD)	14.74	
M373 A5	H-P1131	ATP synthase F1, subunit epsilon (atpC)	13.75	
M373 B5	H-P1134	ATP synthase F1, subunit alpha (atpA)	55.44	
M373 C5	H-P1135	ATP synthase F1, subunit delta (atpH)	19.91	
M373 D5	H-P1137	ATP synthase F0, subunit b' (atpF')	15.95	
M373 E5	H-P1138	plasmid replication-partition related protein	32.01	
M373 F5	H-P1139	SpoOJ regulator (soj)	29.15	
M373 G5	H-P1140	biotin operon repressor/biotin acetyl coenzyme A carboxylase synthetase (birA)	23.43	
M373 H5	H-P1141	methionyl-tRNA formyltransferase (fmt)	33.44	
M373 A6	H-P1144	hypothetical protein	9.46	
M373 B6	H-P1145	hypothetical protein	11.44	
M373 C6	H-P1147	ribosomal protein L19 (rpl19)	13.09	
M373 D6	H-P1148	tRNA (guanine-N1)-methyltransferase (trmD)	25.3	
M373 E6	H-P1149	conserved hypothetical protein	20.35	
M380 F3	H-P1150-2	hypothetical protein	12.76	
M373 F6	H-P1152	signal recognition particle protein (ffh)	49.39	
M380 G3	H-P1153-2	valyl-tRNA synthetase (valS)	96.25	
M380 E3	H-P1157-2	outer membrane protein (omp26)	135.41	
M373 G6	H-P1158	pyrroline-5-carboxylate reductase (proC)	28.38	
M373 H6	H-P1159	cell filamentation protein (fic)	19.58	
M373 A7	H-P1160	conserved hypothetical protein	15.51	
M380 A4	H-P1163-2	hypothetical protein	7.04	
M373 B7	H-P1165	tetracycline resistance protein tetA(P), putative	42.57	
M373 C7	H-P1168	carbon starvation protein (cstA)	75.68	
M373 D7	H-P1169	glutamine ABC transporter, permease protein (glnP)	23.98	
M380 H3	H-P1169-2	glutamine ABC transporter, permease protein (glnP)	23.98	
M374 A1	H-P1170	glutamine ABC transporter, permease protein (glnP)	24.64	
M374 B1	H-P1171	glutamine ABC transporter, ATP-binding protein (glnQ)	27.39	
M374 C1	H-P1172	glutamine ABC transporter, periplasmic glutamine-binding protein (glnH)	30.58	
M374 D1	H-P1173	hypothetical protein	20.24	
M374 E1	H-P1174	glucose/galactose transporter (gluP)	44.88	

M374 F1	H-P1175	conserved hypothetical integral membrane protein	47.96	
M374 G1	H-P1177	outer membrane protein (omp27)	70.62	
M374 H1	H-P1178	purine-nucleoside phosphorylase (deoD)	25.74	
M374 A2	H-P1179	phosphopentomutase (deoB)	45.54	
M374 B2	H-P1180	pyrimidine nucleoside transport protein (nupC)	46.09	
M374 C2	H-P1183	NA ⁺ /H ⁺ antiporter (napA)	42.24	
M374 D2	H-P1184	conserved hypothetical integral membrane protein	50.6	
M374 E2	H-P1185	conserved hypothetical integral membrane protein	43.12	
M374 F2	H-P1186	carbonic anhydrase	22.33	
M374 G2	H-P1187	hypothetical protein	42.46	
M374 H2	H-P1188	hypothetical protein	29.7	
M374 A3	H-P1189	aspartate-semialdehyde dehydrogenase (asd)	38.17	
M374 B3	H-P1191	ADP-heptose-lps heptosyltransferase II (rfaF)	38.5	
M374 C3	H-P1196	ribosomal protein S7 (rps7)	17.16	
M374 D3	H-P1200	ribosomal protein L10 (rpl10)	18.15	
M374 E3	H-P1201	ribosomal protein L1 (rpl1)	25.85	
M374 F3	H-P1202	ribosomal protein L11 (rpl11)	15.62	
M374 G3	H-P1203	transcription termination factor NusG (nusG)	19.47	
M380 B4	H-P1205-2	translation elongation factor EF-Tu (tufB)	44	
M374 H3	H-P1206	multidrug resistance protein (hetA)	63.69	
M374 A4	H-P1207	hypothetical protein	24.53	
M374 B4	H-P1210	serine acetyltransferase (cysE)	18.92	
M380 F4	H-P1213-2	polynucleotide phosphorylase (pnp)	75.79	
M380 G4	H-P1214-2	conserved hypothetical protein	26.51	
M380 C4	H-P1215-2	hypothetical protein	8.91	
M380 D4	H-P1216-2	conserved hypothetical secreted protein	72.71	
M380 E4	H-P1217-2	hypothetical protein	17.6	
M374 C4	H-P1220	ABC transporter, ATP-binding protein (yhcg)	25.19	
M374 D4	H-P1221	conserved hypothetical protein	25.85	
M374 E4	H-P1222	D-lactate dehydrogenase (dld)	104.39	
M374 F4	H-P1224	uroporphyrinogen III cosynthase (hemD)	24.97	
M374 G4	H-P1225	conserved hypothetical integral membrane protein	14.41	
M374 H4	H-P1226	oxygen-independent coproporphyrinogen III oxidase (hemN)	38.83	
M380 H4	H-P1227-2	cytochrome c553	10.67	
M380 A5	H-P1228-2	invasion protein (invA)	17.16	
M380 B5	H-P1229-2	aspartokinase (lysC)	44.66	

M374 A5	H-P1230	hypothetical protein	19.91	
M374 B5	H-P1231	DNA polymerase III delta prime subunit (holB)	24.09	
M374 C5	H-P1232	dihydropteroate synthase (folP)	41.91	
M380 D5	H-P1233-2	hypothetical protein	16.94	
M374 D5	H-P1234	conserved hypothetical integral membrane protein	32.89	
M374 E5	H-P1235	conserved hypothetical integral membrane protein	45.76	
M374 F5	H-P1236	hypothetical protein	20.24	
M374 G5	H-P1237	carbamoyl-phosphate synthetase (pyrAa)	41.36	
M374 H5	H-P1240	conserved hypothetical protein	21.01	
M380 C5	H-P1241-2	alanyl-tRNA synthetase (alaS)	93.28	
M374 A6	H-P1242	conserved hypothetical protein	8.47	
M380 H5	H-P1243-2	outer membrane protein (omp28)	80.74	
M374 B6	H-P1244	ribosomal protein S18 (rps18)	9.46	
M374 C6	H-P1245	single-strand DNA-binding protein (ssb)	19.8	
M374 D6	H-P1246	ribosomal protein S6 (rps6)	15.73	
M380 A6	H-P1247-2	hypothetical protein	37.51	
M374 E6	H-P1248	virulence associated protein homolog (vacB)	70.95	
M380 B6	H-P1249-2	shikimate 5-dehydrogenase (aroE)	29.04	
M380 E5	H-P1251-2	oligopeptide ABC transporter, permease protein (oppB)	38.39	
M380 F5	H-P1252-2	oligopeptide ABC transporter, periplasmic oligopeptide-binding protein (oppA)	65.45	
M380 G5	H-P1253-2	tryptophanyl-tRNA synthetase (trpS)	37.4	
M374 F6	H-P1254	biotin synthesis protein (bioC)	26.51	
M374 G6	H-P1255	protein translocation protein, low temperature (secG)	22.22	
M374 H6	H-P1256	ribosome releasing factor (fir)	20.46	
M374 A7	H-P1257	orotate phosphoribosyltransferase (pyrE)	22.22	
M374 B7	H-P1258	conserved hypothetical mitochondrial protein 4	17.05	
M374 C7	H-P1260	NADH-ubiquinone oxidoreductase, NQO7 subunit (NQO7)	14.74	
M374 D7	H-P1262	NADH-ubiquinone oxidoreductase, NQO5 subunit (NQO5)	29.37	
M374 E7	H-P1263	NADH-ubiquinone oxidoreductase, NQO4 subunit (NQO4)	45.1	
M380 C6	H-P1264-2	hypothetical protein	8.47	
M374 F7	H-P1265	hypothetical protein	36.19	
M375 A1	H-P1268	NADH-ubiquinone oxidoreductase, NQO9 subunit (NQO9)	24.31	

M375 B1	H-P1275	phosphomannomutase (algC)	50.6	
M375 C1	H-P1277	tryptophan synthase, alpha subunit (trpA)	28.93	
M375 D1	H-P1278	tryptophan synthase, beta subunit (trpB)	43.34	
M375 E1	H-P1279	anthranilate isomerase (trpC)	49.83	
M375 F1	H-P1282	anthranilate synthase component I (trpE)	55.11	
M375 G1	H-P1285	conserved hypothetical secreted protein	25.41	
M375 H1	H-P1286	conserved hypothetical secreted protein	20.13	
M375 A2	H-P1287	transcriptional regulator (tenA)	23.98	
M375 B2	H-P1288	hypothetical protein	14.63	
M375 C2	H-P1289	hypothetical protein	17.82	
M375 D2	H-P1290	nicotinamide mononucleotide transporter (pnuC)	24.31	
M375 E2	H-P1291	conserved hypothetical protein	22.55	
M375 F2	H-P1292	ribosomal protein L17 (rpl17)	12.87	
M375 G2	H-P1293	DNA-directed RNA polymerase, alpha subunit (rpoA)	37.95	
M375 H2	H-P1294	ribosomal protein S4 (rps4)	22.99	
M375 A3	H-P1295	ribosomal protein S11 (rps11)	14.52	
M375 B3	H-P1296	ribosomal protein S13 (rps13)	13.31	
M380 D6	H-P1298-2	translation initiation factor EF-1 (infA)	8.03	
M375 C3	H-P1299	methionine amino peptidase (map)	27.94	
M375 D3	H-P1302	ribosomal protein S5 (rps5)	16.94	
M375 E3	H-P1303	ribosomal protein L18 (rpl18)	13.2	
M375 F3	H-P1305	ribosomal protein S8 (rps8)	14.52	
M375 G3	H-P1307	ribosomal protein L5 (rpl5)	20.02	
M375 H3	H-P1308	ribosomal protein L24 (rpl24)	8.14	
M375 A4	H-P1309	ribosomal protein L14 (rpl14)	13.53	
M375 B4	H-P1310	ribosomal protein S17 (rps17)	9.57	
M375 C4	H-P1312	ribosomal protein L16 (rpl16)	15.62	
M375 D4	H-P1314	ribosomal protein L22 (rpl22)	13.53	
M375 E4	H-P1315	ribosomal protein S19 (rps19)	10.34	
M375 F4	H-P1318	ribosomal protein L4 (rpl4)	23.76	
M375 G4	H-P1319	ribosomal protein L3 (rpl3)	21.12	
M375 H4	H-P1320	ribosomal protein S10 (rps10)	11.55	
M375 A5	H-P1321	conserved hypothetical ATP-binding protein	41.58	
M375 B5	H-P1322	hypothetical protein	22.22	
M375 C5	H-P1323	ribonuclease HII (rnhB)	23.1	
M375 D5	H-P1324	hypothetical protein	9.24	
M375 E5	H-P1326	hypothetical protein	13.86	
M375 F5	H-P1327	hypothetical protein	45.43	
M375 G5	H-P1328	cation efflux system protein (czcA)	37.29	
M375 H5	H-P1330	conserved hypothetical integral membrane protein	12.76	

M375 A6	H-P1331	conserved hypothetical integral membrane protein	25.19	
M375 B6	H-P1332	co-chaperone and heat shock protein (dnaJ)	40.7	
M375 C6	H-P1333	hypothetical protein	42.13	
M375 D6	H-P1335	conserved hypothetical protein	39.71	
M375 E6	H-P1336	hypothetical protein	27.94	
M375 F6	H-P1337	conserved hypothetical protein	19.25	
M375 G6	H-P1338	conserved hypothetical protein	16.39	
M375 H6	H-P1340	biopolymer transport protein (exbD)	14.3	
M375 A7	H-P1341	siderophore-mediated iron transport protein (tonB)	31.46	
M375 B7	H-P1342	outer membrane protein (omp29)	76.12	
M375 C7	H-P1343	conserved hypothetical integral membrane protein	26.73	
M375 D7	H-P1344	magnesium and cobalt transport protein (corA)	35.09	
M375 E7	H-P1345	phosphoglycerate kinase	44.33	
M375 F7	H-P1346	glyceraldehyde-3-phosphate dehydrogenase (gap)	36.41	
M375 G7	H-P1347	uracil-DNA glycosylase (ung)	25.74	
M375 H7	H-P1349	hypothetical protein	42.68	
M375 A8	H-P1350	protease	50.6	
M375 B8	H-P1355	nicotinate-nucleotide pyrophosphorylase (nadC)	30.14	
M375 C8	H-P1356	quinolinate synthetase A (nadA)	37.07	
M375 D8	H-P1357	phosphatidylserine decarboxylase proenzyme (psd)	29.48	
M375 E8	H-P1358	hypothetical protein	18.59	
M375 F8	H-P1360	4-hydroxybenzoate octaprenyltransferase (ubiA)	32.45	
M375 G8	H-P1361	competence locus E (comE3)	45.98	
M375 H8	H-P1362	replicative DNA helicase (dnaB)	53.79	
M375 A9	H-P1363	conserved hypothetical integral membrane protein	51.37	
M376 A1	H-P1364	signal-transducing protein, histidine kinase	43.78	
M376 B1	H-P1365	response regulator	23.54	
M376 C1	H-P1371	type III restriction enzyme R protein	106.59	
M376 D1	H-P1372	rod shape-determining protein (mreC)	27.39	
M376 E1	H-P1373	rod shape-determining protein (mreB)	38.28	
M376 F1	H-P1374	ATP-dependent protease ATPase subunit (clpX)	49.17	
M376 G1	H-P1375	UDP-N-acetylglucosamine acyltransferase (lpxA)	29.81	
M376 H1	H-P1376	(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase (fabZ)	17.6	
M376 A2	H-P1377	hypothetical protein	16.17	

M376 B2	H-P1378	competence lipoprotein (comL)	24.31	
M376 C2	H-P1379	ATP-dependent protease (lon)	91.96	
M376 D2	H-P1380	prephenate dehydrogenase (tyrA)	29.26	
M381 C1	H-P1381	hypothetical protein	8.58	
M376 E2	H-P1382	hypothetical protein	14.41	
M376 F2	H-P1383	restriction modification system S subunit	17.71	
M376 G2	H-P1384	hypothetical protein	7.59	
M376 H2	H-P1385	fructose-1,6-bisphosphatase	32.01	
M376 A3	H-P1386	D-ribulose-5-phosphate 3 epimerase (rpe)	23.98	
M376 B3	H-P1388	hypothetical protein	16.5	
M376 C3	H-P1389	hypothetical protein	6.71	
M376 D3	H-P1390	hypothetical protein	18.37	
M376 E3	H-P1391	hypothetical protein	10.89	
M376 F3	H-P1392	fibronectin/fibrinogen-binding protein	47.96	
M376 G3	H-P1393	DNA repair protein (recN)	57.75	
M376 H3	H-P1394	conserved hypothetical protein	31.35	
M376 A4	H-P1395	outer membrane protein (omp30)	26.73	
M376 B4	H-P1396	hypothetical protein	31.79	
M376 C4	H-P1398	alanine dehydrogenase (ald)	41.91	
M376 D4	H-P1399	arginase (rocF)	35.53	
M376 E4	H-P1400	iron(III) dicitrate transport protein (fecA)	92.73	
M376 F4	H-P1401	conserved hypothetical protein	25.96	
M381 A2	H-P1402	type I restriction enzyme R protein (hsdR)	109.34	
M381 B2	H-P1403	type I restriction enzyme M protein (hsdM)	89.98	
M376 G4	H-P1405	hypothetical protein	3.85	
M376 H4	H-P1406	biotin synthetase (bioB)	31.13	
M376 A5	H-P1407	conserved hypothetical integral membrane protein	32.23	
M381 C2	H-P1408	hypothetical protein	12.32	
M381 D2	H-P1409	hypothetical protein	63.69	
M376 B5	H-P1410	hypothetical protein	43.45	
M376 C5	H-P1411	hypothetical protein	68.2	
M376 D5	H-P1412	hypothetical protein	33.99	
M376 E5	H-P1413	conserved hypothetical protein	16.39	
M376 F5	H-P1414	conserved hypothetical protein	12.54	
M376 G5	H-P1415	tRNA delta(2)-isopentenylpyrophosphate transferase (miaA)	29.37	
M376 H5	H-P1418	UDP-N-acetylenolpyruvoylglucosamine reductase (murB)	28.6	
M376 A6	H-P1419	flagellar biosynthetic protein (fliQ)	9.79	
M376 B6	H-P1420	flagellar export protein ATP synthase (fliI)	47.85	
M376 C6	H-P1421	conjugative transfer regulon protein (trbB)	33.55	

M376 D6	H-P1423	conserved hypothetical protein	9.35	
M376 E6	H-P1424	hypothetical protein	22.77	
M376 F6	H-P1425	hypothetical protein	8.36	
M376 G6	H-P1427	histidine-rich, metal binding polypeptide (hpn)	6.71	
M376 H6	H-P1428	conserved hypothetical protein	39.38	
M376 A7	H-P1429	polysialic acid capsule expression protein (kpsF)	36.3	
M376 B7	H-P1430	conserved hypothetical ATP-binding protein	75.9	
M376 C7	H-P1431	16S rRNA (adenosine-N6,N6--dimethyltransferase (ksgA)	29.92	
M376 D7	H-P1432	histidine and glutamine-rich protein	8.03	
M376 E7	H-P1433	hypothetical protein	94.27	
M376 F7	H-P1434	formyltetrahydrofolate hydrolase (purU)	32.34	
M376 G7	H-P1435	protease IV (PspA)	32.23	
M376 H7	H-P1436	hypothetical protein	9.13	
M376 A8	H-P1438	conserved hypothetical lipoprotein	37.29	
M376 B8	H-P1439	hypothetical protein	9.02	
M376 C8	H-P1440	hypothetical protein	28.6	
M376 D8	H-P1441	peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rotamase (ppi)	18.04	
M376 E8	H-P1442	carbon storage regulator (csrA)	8.47	
M376 F8	H-P1443	conserved hypothetical protein	29.59	
M376 G8	H-P1444	small protein (smpB)	16.83	
M376 H8	H-P1445	biopolymer transport protein (exbB)	16.61	
M376 A9	H-P1446	biopolymer transport protein (exbD)	14.74	
M376 B9	H-P1447	ribosomal protein L34 (rpl34)	4.95	
M376 C9	H-P1448	ribonuclease P, protein component (rnpA)	17.82	
M376 D9	H-P1449	conserved hypothetical protein	12.98	
M376 E9	H-P1450	60 kDa inner-membrane protein	60.28	
M376 F9	H-P1451	hypothetical protein	29.15	
M376 G9	H-P1452	thiophene and furan oxidizer (tdhF)	50.82	
M376 H9	H-P1453	conserved hypothetical protein	82.17	
M376 A10	H-P1454	hypothetical protein	33.44	
M376 B10	H-P1455	hypothetical protein	14.41	
M376 C10	H-P1456	membrane-associated lipoprotein (lpp20)	19.36	
M376 D10	H-P1457	hypothetical protein	23.21	
M376 E10	H-P1458	thioredoxin	11.55	
M376 F10	H-P1461	cytochrome c551 peroxidase	38.61	
M377 A1	H-P1462	secreted protein involved in flagellar motility	19.03	
M377 B1	H-P1463	hypothetical protein	24.86	

M377 C1	H-P1464	conserved hypothetical secreted protein	29.92	
M377 D1	H-P1465	ABC transporter, ATP-binding protein (HI1087)	28.82	
M377 E1	H-P1466	conserved hypothetical integral membrane protein	41.58	
M377 F1	H-P1467	hypothetical protein	25.52	
M377 G1	H-P1468	branched-chain-amino-acid aminotransferase (ilvE)	37.51	
M377 H1	H-P1469	outer membrane protein (omp31)	27.39	
M377 A2	H-P1473	hypothetical protein	21.12	
M377 B2	H-P1474	thymidylate kinase (tnk)	21.12	
M377 C2	H-P1475	lipopolysaccharide core biosynthesis protein (kdtB)	17.38	
M377 D2	H-P1476	phenylacrylic acid decarboxylase	20.68	
M377 E2	H-P1479	hypothetical protein	92.95	
M377 F2	H-P1480	seryl-tRNA synthetase (serS)	45.76	
M377 G2	H-P1481	hypothetical protein	29.26	
M377 H2	H-P1482	hypothetical protein	9.57	
M377 A3	H-P1483	gerC2 protein (gerC2)	27.17	
M377 B3	H-P1484	conserved hypothetical integral membrane protein	16.39	
M377 C3	H-P1485	proline dipeptidase (pepQ)	21.01	
M377 D3	H-P1486	conserved hypothetical integral membrane protein	41.47	
M377 E3	H-P1487	conserved hypothetical integral membrane protein	40.26	
M377 F3	H-P1488	conserved hypothetical secreted protein	36.3	
M377 G3	H-P1489	lipase-like protein	56.21	
M381 G1	H-P1490	hemolysin	49.5	
M377 H3	H-P1491	phosphate permease	58.74	
M377 A4	H-P1492	conserved hypothetical nifU-like protein	9.9	
M377 B4	H-P1493	hypothetical protein	22.44	
M377 C4	H-P1494	UDP-MurNac-tripeptide synthetase (murE)	49.28	
M377 D4	H-P1495	transaldolase (tal)	34.87	
M377 E4	H-P1496	general stress protein (ctc)	19.69	
M377 F4	H-P1497	peptidyl-tRNA hydrolase (pth)	20.57	
M377 G4	H-P1499	hypothetical protein	30.03	
M377 H4	H-P1501	outer membrane protein (omp32)	42.79	
M377 A5	H-P1502	hypothetical protein	16.06	
M377 B5	H-P1503	cation-transporting ATPase, P-type (copA)	86.79	
M377 C5	H-P1504	conserved hypothetical protein	26.29	
M377 D5	H-P1505	riboflavin biosynthesis protein (ribG)	37.95	
M377 E5	H-P1506	glutamate permease (gltS)	44.99	
M377 F5	H-P1507	conserved hypothetical ATP-binding protein	42.46	
M381 F2	H-P1508	ferredoxin-like protein	50.49	

M377 G5	H-P1509	conserved hypothetical integral membrane protein	28.93	
M377 H5	H-P1510	conserved hypothetical protein	12.98	
M377 A6	H-P1511	hypothetical protein	11.99	
M377 B6	H-P1512	iron-regulated outer membrane protein (frpB)	96.58	
M377 C6	H-P1513	selenocystein synthase (selA)	42.57	
M377 D6	H-P1514	transcription termination factor NusA (nusA)	43.56	
M377 E6	H-P1518	hypothetical protein	10.56	
M381 B3	H-P1521	type III restriction enzyme R protein (res)	106.48	
M381 C3	H-P1523	DNA recombinase (recG)	68.64	
M377 F6	H-P1524	hypothetical protein	12.76	
M377 G6	H-P1525	hypothetical protein	23.32	
M377 H6	H-P1526	exodeoxyribonuclease (lexA)	27.61	
M377 A7	H-P1527	hypothetical protein	52.8	
M377 B7	H-P1530	purine nucleoside phosphorylase (punB)	19.91	
M377 C7	H-P1531	hypothetical protein	8.8	
M377 D7	H-P1532	glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS)	65.78	
M377 E7	H-P1533	conserved hypothetical protein	25.52	
M377 F7	H-P1534	IS605 transposase (tnpB)	47.08	
M377 G7	H-P1535	IS605 transposase (tnpA)	15.73	
M377 H7	H-P1541	transcription-repair coupling factor (trcF)	110	
M377 A8	H-P1548	conserved hypothetical integral membrane protein	12.43	
M377 B8	H-P1551	conserved hypothetical secreted protein	14.08	
M377 C8	H-P1552	Na ⁺ /H ⁺ antiporter (nhaA)	48.29	
M381 B4	H-P1554	ribosomal protein S2 (rps2)	29.15	
M381 D4	H-P1555	translation elongation factor EF-Ts (tsf)	39.16	
M377 D8	H-P1556	cell division protein (ftsI)	67.76	
M381 E4	H-P1557	flagellar basal-body protein (fliE)	12.1	
M381 F4	H-P1558	flagellar basal-body rod protein (flgC) (proximal rod protein)	17.82	
M381 G4	H-P1559	flagellar basal-body rod protein (flgB) (proximal rod protein)	15.51	
M378 A1	H-P1560	cell division protein (ftsW)	42.79	
M378 B1	H-P1561	iron(III) ABC transporter, periplasmic iron-binding protein (ceuE)	36.96	
M378 C1	H-P1562	iron(III) ABC transporter, periplasmic iron-binding protein (ceuE)	36.74	
M378 D1	H-P1563	alkyl hydroperoxide reductase (tsaA)	21.89	
M378 E1	H-P1564	outer membrane protein	29.92	

M378 F1	H-P1565	penicillin-binding protein 2 (pbp2)	64.79	
M378 G1	H-P1566	hypothetical protein	16.28	
M378 H1	H-P1567	conserved hypothetical ATP-binding protein	22.99	
M378 A2	H-P1568	hypothetical protein	20.24	
M378 B2	H-P1569	hypothetical protein	21.78	
M378 C2	H-P1570	conserved hypothetical protein	18.15	
M378 D2	H-P1571	rare lipoprotein A (rlpA)	34.76	
M378 E2	H-P1572	regulatory protein DniR	41.03	
M378 F2	H-P1573	conserved hypothetical protein	28.05	
M378 G2	H-P1576	ABC transporter, ATP-binding protein (abc)	36.08	
M378 H2	H-P1577	ABC transporter, permease protein (yaeE)	23.76	
M378 A3	H-P1580	hypothetical protein	24.31	
M378 B3	H-P1581	methicillin resistance protein (ilm)	37.07	
M378 C3	H-P1582	pyridoxal phosphate biosynthetic protein J (pdxJ)	28.93	
M378 D3	H-P1583	pyridoxal phosphate biosynthetic protein A (pdxA)	33.88	
M378 E3	H-P1584	sialoglycoprotease (gcp)	37.51	
M378 F3	H-P1585	flagellar basal-body rod protein (flgG)	28.93	
M378 G3	H-P1587	conserved hypothetical protein	17.16	
M378 H3	H-P1588	conserved hypothetical protein	27.94	
M381 H1	H-P1590	hypothetical protein	4.4	
M318 G2	H-S38729	autoimmune antigen Ku, p70 subunit	67.1	67
H1	H-S39329	Kallikrein 1 (renal/pancreas/salivary) {alternative products}	24.64	30
M270 G4	H-S43855	Recoverin, photoreceptor protein	22.11	32.0kDa
M300 C2	H-S56151	milk fat globule protein HMFG	24.09	30
M318 C1	H-S57153	retinoblastoma-binding protein 1, isoform I [RBBP1]	101.31	101
M271 B2	H-S57162	retinoblastoma-binding protein 1, isoform III [RBBP1], INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE RETINOBLASTOMA PROTEIN.	93.72	110
M317 H3	H-S62027	transducin, gamma subunit	8.25	11
M270 G6	H-S66793	arrestin, X-arrestin=S-antigen homolog [human, retina, mRNA, 1314 nt], MAY PLAY A ROLE IN AN AS YET UNDEFINED RETINA-SPECIFIC SIGNAL TRANSDUCTION.	42.79	50.0kDa
M419 C2	H-S67859	"transcription initiation factor IIE, alpha subunit"	48.360	64.0kDa

M302 D7	H-S69022	myosin, light polypeptide 2, ventricular	18.26	31
H5	H-S69272	cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt]	41.47	50
D1	H-S72043	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]	7.59	19
M266 B3	H-S74221	cytokine IK factor	17.93	36.0kDa
D1	H-S74445	cellular retinoic acid-binding protein [human, skin, mRNA, 735 nt]	15.18	23
E3	H-S74728	antiquitin=26g turgor protein homolog [human, kidney, mRNA, 1809 nt]	56.32	53
D4	H-S75174	E2F transcription factor 4, p107/p130-binding	45.87	58
166-61	H-S76474	"trkB {alternately spliced} [human, brain, mRNA]"	55	52.54
169-40	H-S76617	"B1k=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]"	60	55.62
M250 D3	H-S79522	ubiquitin carboxyl-terminal extension protein, Ubiquitin A-52 residue ribosomal protein fusion product 1	17.27	17.0kDa
M236 B4	H-S80562	calponin, acidic	36.3	49
G1	H-S82470	BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]	37.73	34
M313 E1	H-S85655	prohibitin [PHB]	30.03	40.0kDa
M465 A6	H-S87759	protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]	42.13	52.0kDa
M472 B1	H-U00803	tyrosine-protein kinase FRK	55.620	64.0kDa
B2	H-U02390	Human adenylyl cyclase-associated protein homolog CAP2 (CAP2) mRNA, complete cds	52.58	55
167-2	H-U02680	human protein tyrosine kinase mRNA	36	38.57
G2	H-U03056	Human tumor suppressor (LUCA-1) mRNA, complete cds	47.96	47
M512 E3	H-U03100	Human alpha2(E)-catenin mRNA, complete cds	102.52	102.0kDa
M306 G3	H-U03187		72.93	95.0kDa
H3	H-U03398	Human receptor 4-1BB ligand mRNA, complete cds	28.05	51
D3	H-U03486	Human connexin40 gene, complete cds	39.49	40
M300 C3	H-U03643	leukophysin	25.96	34

F5	H-U03749	Human chromogranin A (CHGA) gene, promoter and	50.38	50
M314 C3	H-U03886	GS2 (GB:U03886)	27.94	32.0kDa
M306 E3	H-U04343	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen) [CD86]	35.64	47
167-61	H-U05012	TrkC	92	90.82
M302 G5	H-U05340	cell division cycle protein p55	55	55
A4	H-U05659	Hydroxysteroid (17-beta) dehydrogenase 3	34.21	36
F1	H-U05861	Human hepatic dihydriol dehydrogenase gene	35.64	40
M302 B2	H-U06452	antigen MART-1, melanoma	13.09	20.0kDa
169-52	H-U06454	human AMP-activated protein kinase (hAMPK) mRNA	70	60.79
M315 A3	H-U06643	lectin, epidermal	15.07	18
H1	H-U06715	Cytochrome B561	27.06	25
M476 E5	H-U07132	Human steroid hormone receptor Ner-I mRNA, complete cds	50.82	55.0kDa
M236 D3	H-U07151	guanine nucleotide-binding protein ADP-ribosylation factor like gene 3	20.13	34
M317 G3	H-U07559	homeotic protein Islet-1	38.17	38
M266 H1	H-U07681	Human NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds	40.37	40
E3	H-U07919	Aldehyde dehydrogenase 6	56.43	53
M298 A3	H-U08021	nicotinamide N-methyltransferase	29.15	36.0kDa
M297 B1	H-U08024	alcohol/hydroxysteroid sulfotransferase	31.46	50.0kDa
A2	H-U08336	Human basic helix-loop-helix transcription factor mRNA, complete cds	21.89	42
E2	H-U09303	Human T cell leukemia LERK-2 (EPLG2) mRNA, complete cds	38.17	40
M250 H5	H-U09559	RCH1, RAG (recombination activating gene) cohort 1	58.3	58.0kDa
167-50	H-U09564	human serine kinase mRNA	72	72.12
166-74	H-U09578	human MAPKAP kinase (3pK) mRNA	50	42.09
M302 C4	H-U09813	ATP synthase, subunit 9, mitochondrial	15.73	30
A1	H-U09850	Zinc finger protein 143 (clone pHZ-1)	68.97	68
M423 E1	H-U09937	Human urokinase-type plasminogen receptor	36.96	49.0kDa
M450 H4	H-U10117	Human endothelial-monocyte activating polypeptide II mRNA, complete cds	34.43	38.0kDa
M314 G1	H-U10248	ribosomal protein L29	17.6	27
M298 H1	H-U10323	nuclear factor 45	44.77	45
E1	H-U10492	Human Mox1 protein (MOX1) mRNA, complete cds	28.05	37

F3	H-U10686	Human MAGE-11 antigen (MAGE11) gene, complete cds	35.2	35
167-38	H-U11050	human NIMA-like protein kinase 1 (NLK1) mRNA	55	49.02
M266 B2	H-U11292	Human Ki nuclear autoantigen mRNA, complete cds, may play a rol in cell adhesion	29.48	32
167-62	H-U11791	human cyclin H m RNA	40	35.60
M423 D5	H-U12255	immunoglobulin gamma heavy chain Fc receptor RI, high affinity	40.26	48.0kDa
M302 F7	H-U12404	Csa-19	23.98	32
M236 A2	H-U12465	ribosomal protein L35	13.64	24
169-4	H-U12535	human epidermal growth factor receptor kinase substrate (Eps8) mRNA	100	90.49
F3	H-U12597	Human tumor necrosis factor type 2 receptor associated protein (TRAP3) mRNA, complete cds	55.22	64
M314 D1	H-U12979	transcriptional coactivator PC4	14.08	23
M476 G4	H-U13044	GA-binding protein transcription factor, alpha subunit (60kD)	50.05	53.0kDa
M302 F3	H-U13665	cathepsin O (GB:U13665)	36.3	50.0kDa
M311 G4	H-U13831	cellular retinol binding protein II	14.85	20.0kDa
A2	H-U13991	Human TATA-binding protein associated factor 30 kDa subunit (tafII30) mRNA, complete cds	24.09	34
M416 A4	H-U14187	Human receptor tyrosine kinase ligand LERK-3 (EPLG3) mRNA, complete cds	26.29	29.0kDa
M250 A2	H-U14188	eph-related receptor tyrosine kinase ligand 4 [EPLG4]	22.22	27
M302 D2	H-U14193	human TFIIA gamma subunit mRNA	12.060	28.0kDa
M416 G1	H-U14603	Human protein-tyrosine phosphatase (HU-PP-1) mRNA, partial sequence	18.48	30.0kDa
E2	H-U14747	Visinin-like 1	21.12	25
M266 D4	H-U14966	ribosomal protein L5	32.78	38
M314 E2	H-U14967	ribosomal protein L21	17.71	29
M266 F5	H-U14968	ribosomal protein L27a	16.39	19.0kDa
M248 E3	H-U14969	ribosomal protein L28	15.18	27
M266 E1	H-U14971	ribosomal protein S9	21.45	30
M250 C2	H-U15009	small nuclear ribonucleoprotein, Sm D3	13.97	17.0kDa
M311 D4	H-U16660	enoyl-Coenzyme A hydratase-like protein, peroxisomal	36.19	38
M302 H4	H-U17074	cyclin-dependent kinase 6 inhibitor p18	18.59	29
M306 A2	H-U17195	A-kinase anchor protein 100 [AKAP100*]	72.05	100
D1	H-U17280	Steroidogenic acute regulatory protein	31.46	35
M316 F1	H-U18291	cell division cycle protein 16	68.2	71.0kDa

C5	H-U18420	Human ras-related small GTP binding protein Rab5 (rab5) mRNA, complete cds	23.87	33
M311 A2	H-U18423	spinal muscular atrophy gene	32.45	41
M248 D4	H-U18914	hypothetical protein, (Human 19.8 kDa protein mRNA, complete cds)	20.35	32
M302 B5	H-U19718	microfibril-associated glycoprotein 2	20.24	34.0kDa
M305 E3	H-U20240	CCAAT/enhancer-binding protein gamma	16.61	29
M302 A8	H-U20352	malate dehydrogenase	36.85	40
M416 F4	H-U20391	Human folate receptor (FOLR1) gene, complete cds	28.38	34.0kDa
M311 D1	H-U20536	apoptotic cysteine protease Mch2	32.34	38.0kDa
M431 G2	H-U20659	RNA polymerase II, subunit B7	19.03	31.0kDa
M499 C1	H-U20938	Human lymphocyte dihydropyrimidine dehydrogenase mRNA, complete cds	112.86	100.0kDa
M305 F2	H-U20972	14-3-3 protein, epsilon	28.16	36
M271 D3	H-U21049	hypothetical protein (GB:U21049), ESTs, Highly similar to DD96 [H.sapiens].	12.65	16
M421 G5	H-U21858	Human transcriptional activation factor TAFII32 mRNA, complete cds	29.15	38.0kDa
M424 H3	H-U22662	Human nuclear orphan receptor LXR-alpha mRNA, complete cds	49.28	49.0kDa
M271 D2	H-U24074	killer cell inhibitory receptor [KIR], Homo sapiens natural killer-associated transcript 3 (NKAT3), complete cds. RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.	37.62	43
169-29	H-U24153	human p21-activated protein kinase (Pak2) gene	60	57.82
M385 H2	H-U24166	EB1	29.59	36.0kDa
G1	H-U24169	Human JTV-1 (JTV-1) mRNA, complete cds	34.43	40
E1	H-U24576	Human breast tumor autoantigen mRNA, complete sequence	18.26	27
G4	H-U24577	Human LDL-phospholipase A2 mRNA, complete cds	48.62	52
H1	H-U25789	Human ribosomal protein L21 mRNA, complete cds	17.71	32
M416 D1	H-U25849	Human red cell-type low molecular weight acid phosphatase (ACP1) gene, 5' flanking region and	17.49	28.0kDa
M300 A3	H-U26312	heterochromatin protein H-P1Hs-gamma	19.14	30

M416 D3	H-U26403	Human receptor tyrosine kinase ligand LERK-7 precursor (EPLG7) mRNA, complete cds	25.19	30.0kDa
M317 E2	H-U27143	human protein kinase C inhibitor-I cDNA	13.900	17.0kDa
E5	H-U28249	Human 11kd protein mRNA, complete cds	12.32	12
F4	H-U28386	Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds	58.3	54
M423 E3	H-U28694	Chemokine (C-C) receptor 3	39.16	39.0kDa
M266 G6	H-U28963	Gps2	36.08	36
M306 D3	H-U30610	CD94 antigen (NK/T-cell C-type lectin receptor) [CD94]	19.8	27
B1	H-U31116	Human beta-sarcoglycan A3b mRNA, complete cds	35.09	33
M297 C2	H-U31278	mitotic feedback control protein Madp2 homolog	22.66	31.0kDa
M302 G2	H-U31384	guanine nucleotide-binding protein, gamma 11 subunit	8.14	10
F4	H-U31986	Human cartilage-specific homeodomain protein Cart-1 mRNA, complete cds	35.97	47
M390 F3	H-U32114	caveolin 2	17.93	18.0kDa
E4	H-U32324	Human interleukin-11 receptor alpha chain mRNA, complete cds	46.53	54
F1	H-U32576	Apolipoprotein C-IV	14.08	16
M298 C4	H-U32907	p37NB protein	34.54	39
M300 D3	H-U32944	dynein, light chain 1, cytoplasmic	9.9	15
M297 D1	H-U32989	tryptophan 2,3-dioxygenase	44.77	50.0kDa
166-51	H-U33052	"protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA]"	110	108.3
166-64	H-U33054	"human G protein-coupled receptor kinase GRK4 mRNA, alpha splice variant"	52	63.65
166-88	H-U33055	"human G protein-coupled receptor kinase GRK4 mRNA, beta splice variant"	60	60.1
166-76	H-U33056	"human G protein-coupled receptor kinase GRK4 mRNA, gamma splice variant"	58	58.59
A2	H-U34584		17.71	31
169-87	H-U34820	human MAP kinase mRNA	55	46.49
215-2	H-U34822	human JNK1 alpha2 protein kinase (JNK1A2) mRNA	55	47.04
169-37	H-U35002	human JNK2 beta1 protein kinase (JNK2B1) mRNA	50	42.09
169-25	H-U35003	human JNK2 beta2 protein kinase (JNK2B2) mRNA	55	46.71
167-16	H-U35004	human JNK1 beta1 protein kinase (JNK1B1) mRNA	52	42.31
M300 B2	H-U35048	TSC-22 protein	15.95	27

M423 E5	H-U35398	Human G protein-coupled receptor mRNA, complete cds	40.26	48.0kDa
A3	H-U35735	Human RACH1 (RACH1) mRNA, complete cds	42.9	78
M250 E5	H-U36764	Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit, transforming growth factor-beta receptor II interacting protein 1	35.86	36.0kDa
M270 E4	H-U37283	microfibril-associated glycoprotein-2 (GB:U37283)	19.14	32
M426 F3	H-U37352	Protein phosphatase 2A, regulatory subunit B' alpha-1	56.65	55.0kDa
E1	H-U37529	Human substance P beta-PPT-A mRNA, complete cds	14.3	22
M305 H5	H-U37547	apoptosis inhibitor	68.09	64
M424 D5	H-U38480	Human retinoid X receptor-gamma mRNA, complete cds	51.04	61.0kDa
M270 F4	H-U38810	Human mab-21 cell fate-determining protein homolog (CAGR1) mRNA,		
M467 F6	H-U38904	Human zinc finger protein C2H2-25 mRNA, complete cds	40.48	47.0kDa
E2	H-U39318	Human E2 ubiquitin conjugating enzyme UbCH5C (UBCH5C) mRNA, complete cds	16.28	22
166-75	H-U39657	human MAP kinase kinase 6 (MKK6) mRNA	40	36.81
M298 E4	H-U39945	human adenylate kinase 2 (adk2) mRNA	26.3633	38.0kDa
166-38	H-U40282	human integrin-linked kinase (ILK) mRNA	55	49.68
169-65	H-U40343	human CDK inhibitor p19INK4d mRNA	18	18.33
E2	H-U40705	Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds	48.4	52
166-50	H-U40989	human tat interactive protein mRNA	60	53.09
M266 H6	H-U41767	metargidin precursor	89.65	90
M270 F3	H-U41804	Human putative T1/ST2 receptor binding protein precursor mRNA, complete cds	25.08	35.0kDa
D5	H-U42360	Human N33 gene	38.28	38
A1	H-U43368	Vascular endothelial growth factor B	22.88	33
M421 G7	H-U43901	Human 37 kD laminin receptor precursor/p40 ribosome associated protein gene, complete cds	32.56	58.0kDa
M392 C2	H-U43923	transcription factor SUPTH4	12.98	16.0kDa
E2	H-U46024	Myotubular myopathy 1	66.44	58
M330 A1	H-U46838	p105MCM	90.42	97
M476 E2	H-U47677	Human transcription factor E2F1 (E2F1) gene, promoter and	48.18	53.0kDa

M421 H1	H-U48707	Human protein phosphatase-1 inhibitor mRNA, complete cds	18.92	36.0kDa
M302 B7	H-U49070	peptidyl-prolyl isomerase PIN1	18.04	28.0kDa
C1	H-U49188	Human placenta (Diff33) mRNA, complete cds	54.45	70
M485 H2	H-U49837	Human LIM protein MLP mRNA, complete cds	21.45	34.0kDa
D2	H-U49897	Homo sapiens phenylalanine hydroxylase (PAH) mRNA, complete cds	49.83	64
B2	H-U49957	Human LIM protein (LPP) mRNA, partial cds	67.43	67
166-16	H-U50196	human adenosine kinase mRNA	50	38.02
A4	H-U50939	Human amyloid precursor protein-binding protein 1 mRNA, complete cds	58.85	60
G3	H-U51224	Human U2AFBPL gene, complete cds	52.8	55
M486 E3	H-U51333	Hexokinase 3 (white cell)	101.64	100.0kDa
M305 D1	H-U51478	ATPase, Na+/K+ transporting, beta 3 subunit	30.8	36
M416 H3	H-U52112	Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28hu2 gene	25.96	36.0kDa
M463 E1	H-U53442	human p38Beta MAP kinase mRNA	40.99	49.0kDa
G3	H-U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds	84.81	98
M463 C1	H-U54617	human pyruvate dehydrogenase kinase isoform 4 mRNA	45.28	52.0kDa
169-38	H-U54645	methylmalonyl-coA mutase precursor	38	25.59
M300 H3	H-U56255	t-complex sterility protein homolog CW-i	12.54	16
C4	H-U56417	Human lysophosphatidic acid acyltransferase-alpha mRNA, complete cds	31.24	46
M305 A2	H-U56637	actin-capping protein alpha subunit isoform 1	31.57	31

M235 E6	H-U56814	Human DNase1-Like III protein (DNAS1L3) mRNA, complete cds, involved in apoptosis Binds specifically to G-ACTIN AND BLOCKS ACTIN POLYMERIZATION.	33.66	40.0kDa
D5	H-U57059		31.02	36
B3	H-U57093	Human small GTP-binding protein rab27b mRNA, complete cds	24.09	34
D3	H-U57099	Human APEG-1 mRNA, complete cds	12.54	20
F1	H-U58331	Sarcoglycan, delta (35kD dystrophin-associated glycoprotein)	28.27	24
M512 F4	H-U58334	Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA, complete cds	110.66	108.0kDa
B3	H-U58516	Human breast epithelial antigen BA46 mRNA, complete cds	42.68	50
M250 E4	H-U58522	Human huntingtin interacting protein (HIP2) mRNA, complete cds	22.11	30
M419 G2	H-U60207	human stress responsive serine/threonine protein kinase Krs-2 mRNA	53.640	63.0kDa
M298 B2	H-U60276	arsA homolog (hASNA-I)	36.63	47.0kDa
B2	H-U60521	Human protease proMch6 (Mch6) mRNA, complete cds	45.87	52
F3	H-U61166	Human SH3 domain-containing protein SH3P17 mRNA, complete cds	57.31	57
M250 B5	H-U61232	cofactor E (tubulin-folding protein), REQUIRED FOR VIABILITY IN THE ABSENCE OF THE KINESIN-RELATED CIN8		
A5	H-U62392	Homo sapiens zinc finger protein mRNA, complete cds	43.45	52
G1	H-U62801	Human protease M mRNA, complete cds	26.95	33
M266 B1	H-U62962	Int-6 , Human Int-6 mRNA, complete cds	49.06	52.0kDa
M300 G1	H-U63295	seven in absentia homolog	31.13	36
M306 H3	H-U64198		94.93	98
H3	H-U64863	Human hPD-1 (hPD-1) mRNA, complete cds	31.79	37
B3	H-U65581	Human ribosomal protein L3-like mRNA, complete cds	44.88	52
M341 D1	H-U65918	DAZ homologue [DAZLA]	32.56	36.0kDa
M302 E1	H-U65928	Jun activation domain binding protein	36.85	48.0kDa

M512 D3	H-U66347	Homo sapiens cAMP phosphodiesterase (PDE4C) mRNA, 4C-426 isoform, complete cds	46.97	60.0kDa
M306 F3	H-U66867	ubiquitin-conjugating enzyme E2I [UBE2I]	17.49	28
M416 E2	H-U68111	Human protein phosphatase inhibitor 2 (PPP1R2) gene	22.66	37.0kDa
F2	H-U68382	Mannosidase, alpha B, lysosomal	35.64	36
G2	H-U69141	Glutaryl-Coenzyme A dehydrogenase	48.29	56
B2	H-U70660	Human copper transport protein HAH1 (HAH1) mRNA, complete cds	7.59	16
M297 B2	H-U71374	peroxisomal membrane protein (Pex13p)	40.15	40.0kDa
M306 A3	H-U75272	progastricin [PGC]	42.79	49.0kDa
A2	H-U75285	Homo sapiens apoptosis inhibitor survivin gene, complete cds	15.73	25
B2	H-U77456	Human nucleosome assembly protein 2 mRNA, complete cds	41.36	50
C2	H-U78294	Homo sapiens 15S-lipoxygenase mRNA, complete cds	74.47	74
F6	H-U78302	Human 2,4-dienoyl-CoA reductase gene	36.96	40
M478 G3	H-U78798	Human TNF receptor associated factor 6 (TRAF6) mRNA, complete cds	57.53	65.0kDa
G3	H-U80982	Human myeloid-specific C/EBP-epsilon transcription factor (CEBPE) gene, complete cds	27.5	51
M468 B7	H-U82256	Homo sapiens arginase type II mRNA, complete cds	39.05	45.0kDa
M465 B2	H-U82812	Human scavenger receptor cysteine rich Sp alpha mRNA, complete cds	38.28	48.0kDa
M484 D7	H-U83410	Human CUL-2 (cul-2) mRNA, complete cds	82.06	85.0kDa
M467 E6	H-U83460	Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds	21.01	32.0kDa
D2	H-U84763	Homo sapiens UCP3 mRNA, complete cds	34.43	42
B2	H-U86070	Homo sapiens phosphomannomutase mRNA, complete cds	28.93	36
C2	H-U90441	Human prolyl 4-hydroxylase alpha (II) subunit mRNA, complete cds	58.96	64
B2	H-U90543	Human butyrophilin (BTF1) mRNA, complete cds	58.08	54
H2	H-U90545	Human sodium phosphate transporter (NPT4) mRNA, complete cds	44.22	36

G2	H-U90552	Human butyrophilin (BTF5) mRNA, complete cds	56.54	48
C3	H-U91521	Peroxisomal biogenesis factor 12	39.6	48
H1	H-U91641	Human alpha2,8-sialyltransferase mRNA, complete cds	41.47	45
C1	H-U93869	Human RNA polymerase III subunit (RPC39) mRNA, complete cds	34.98	36
F2	H-U94346	Human calpain-like protease (htra-3) mRNA, complete cds	70.4	65
C2	H-U94855	Human translation initiation factor 3 47 kDa subunit mRNA, complete cds	39.38	36
M271 F7	H-U95089	Epidermal growth factor receptor.	44.66	47
M424 A5	H-U95847	Human GDNF receptor alpha mRNA, complete cds	50.71	52.0kDa
D2	H-U96094	Human sarcophilin (SLN) mRNA, complete cds	3.52	10
B3	H-U96769	Homo sapiens chondroadherin gene, 5'flanking region and	39.6	43
M298 G2	H-V00566	prolactin	25.08	35
M298 H2	H-V00571	corticotropin-releasing factor	21.67	49
217-61	H-V00572	phosphoglycerate kinase 1	50	45.94
M314 B3	H-V00597	parathyroid hormone	12.76	14
M305 B8	H-X00129	retinol-binding protein 4, interstitial [RBP4]	22	51
F2	H-X00351	Human mRNA for beta-actin	41.36	41
A4	H-X00570	apolipoprotein C-I	9.24	35
M362 E1	H-X01057	interleukin 2 receptor, alpha [IL2RA]	30.03	40.0kDa
A4	H-X01677P	Human liver mRNA for glyceraldehyde-3-phosphate dehydrogenase (G3PD, EC 1.2.1.12)	10.45	10
M271 D6	H-X02152	lactate dehydrogenase A [LDHA], L-LACTATE DEHYDROGENASE M CHAIN	36.63	45.0kDa
A1	H-X02158	Human gene for erythropoietin	21.34	32
H4	H-X02415	Human gene for fibrinogen gamma chain	48.18	50
A5	H-X02750	Protein C (inactivator of coagulation factors Va and VIIIa)	50.82	53
M302 B3	H-X02751	proto-oncogene N-ras	20.9	25.0kDa
D3	H-X02812	Human mRNA for transforming growth factor-beta (TGF-beta)	43.12	50
M302 C1	H-X03124	tissue inhibitor of metalloproteinase 1	22.88	36.0kDa
M362 B1	H-X03342	ribosomal protein L32	14.96	24.0kDa
M235 A2	H-X03484	human mRNA for raf oncogene	71.350	73.0kDa
M318 A3	H-X03557	interferon-induced protein 56	52.69	50.0kDa
A3	H-X03747	ATPase, Na+/K+ transporting, beta 1 polypeptide	33.44	45

M305 D2	H-X04297	ATPase, Na ⁺ /K ⁺ transporting, alpha subunit	112.64	99
M305 A5	H-X04327	2,3-bisphosphoglycerate mutase	28.6	36
M271 G5	H-X04588	tropomyosin TM30nm, cytoskeletal	26.29	40.0kDa
M305 C8	H-X04741	ubiquitin related protein	23.43	28.0kDa
M236 A5	H-X05231	matrix metalloproteinase 1 (interstitial collagenase) [MMP1], CLEAVES COLLAGENS	51.7	53.0kDa
166-53	H-X05246	"phosphoglycerate kinase, testis specific"	50	45.94
M236 A1	H-X05908	annexin I, REGULATES PHOSPHOLIPASE A2 ACTIVITY, Binds CALCIUM IONS	38.17	40
M250 A4	H-X06234	S100 calcium-binding protein A8 (calgranulin A)	10.34	10.0kDa
M266 B6	H-X06323	ribosomal protein L3, isoform 1	38.39	39
M313 A7	H-X06617	ribosomal protein S11	17.49	27
M416 E4	H-X06948	High affinity IgE receptor alpha-subunit (FcERI)	28.38	36.0kDa
M421 H7	H-X07203	Human mRNA for CD20 receptor (S7)	32.78	40.0kDa
217-2	H-X07743	pleckstrin	38	38.57
217-73	H-X07767	"cAMP-dependent protein kinase, alpha-catalytic subunit"	45	38.68
M305 B3	H-X07898	troponin C, skeletal, fast	17.71	25
M306 E1	H-X07979	integrin, beta 1	87.89	110
A11	H-X08004	ras-related protein rap1B	20.24	38
M235 A7	H-X12387	Cytochrome P450 IIIA3 (nifedipine oxidase chain 3)	55.44	60.0kDa
M315 F1	H-X12496	glycophorin C	14.19	24
M316 D3	H-X12517	small nuclear ribonucleoprotein U1, C	17.6	30.0kDa
M236 E5	H-X12534	guanine nucleotide-binding protein rap2, ras-oncogene related	20.24	34.0kDa
M266 E3	H-X12597	High-mobility group (nonhistone chromosomal) protein 1, placenta	23.76	37
217-14	H-X12656	human mRNA for protein phosphatase 2A (beta type)	40	34.06
H4	H-X12662	H.sapiens arginase gene exon 1 and flanking regions (EC 3.5.3.1) (and joined CDS)	35.53	50
C1	H-X12953	RAB2, member RAS oncogene family	23.43	29
F5	H-X13956	Human 12S RNA induced by poly(rI), poly(rC) and Newcastle disease virus	9.13	19
M297 A1	H-X15005	laminin receptor 1	33.11	48.0kDa
M315 E3	H-X15088	guanine nucleotide binding protein (G protein), alpha transducing (transducin) activity polypeptide 1 [GNAT1]	38.61	45

G2	H-X15183	Human mRNA for 90-kDa heat-shock protein	80.63	80
M385 C1	H-X15422	mannose-binding lectin, soluble (opsonic defect) [MBL]	27.39	27.0kDa
M271 D7	H-X15606	INTERCELLULAR ADHESION MOLECULE-2 PRECURSOR [Homo sapiens].	30.36	37.0kDa
M298 C5	H-X15653	uracil-DNA glycosylase	33.55	37
M302 B4	H-X15822	cytochrome-c oxidase, VIIa subunit, liver	9.24	20
M305 A6	H-X15940	ribosomal protein L31	13.86	18
M236 G5	H-X15949	interferon regulatory factor 2 , BINDS AND REPRESSES REGULATORY REGION OF TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES.	38.5	54.0kDa
M236 C2	H-X16064	translationally-controlled tumor protein	19.03	35
M512 B5	H-X16323	Hepatocyte growth factor (hepapoietin A)	80.19	100.0kDa
M315 C3	H-X16461	cell division cycle 2, G1 to S and G2 to M [CDC2]	32.78	40
M297 G2	H-X16832	cathepsin H	36.96	45.0kDa
M271 B1	H-X16983	integrin, alpha 4 (CD49D, alpha 4 subunit of VLA-4 receptor) [ITGA4], IMPORTANT FOR CELL-CELL ADHESION FUNCTION.	114.29	114
M270 A7	H-X17025	plasminogen activator-inducible c54, Human homolog of yeast IPP isomerase	25.19	34
M302 C3	H-X17042	proteoglycan 1, secretory granule	17.49	26
B1	H-X17206	ribosomal protein S2	24.42	45
B4	H-X17254	Transcription factor Eryf1	45.54	53
M311 H2	H-X17610	beta-1-glycoprotein, pregnancy-specific (GB:X17610)	46.97	48.0kDa
M315 D1	H-X17644	G1 to S phase transition protein (GST1)	55	55
M340 G1	H-X51415	lipase, hormone-sensitive [LIPE]	84.59	98.0kDa
M464 A7	H-X51688	Cyclin A	47.63	47.0kDa
M313 G1	H-X51745	major histocompatibility complex, class I, A	40.26	50
M297 A2	H-X51804	putative receptor protein PMI	21.23	30
D4	H-X51952	Human UCP gene for uncoupling protein exons 1 and 2	33.88	37
M300 B1	H-X52011	muscle determining factor	26.73	39
M419 G1	H-X52479	"protein kinase c, alpha type"	82.28	85.0kDa
A2	H-X52486	Uracil-DNA glycosylase	35.97	36
E3	H-X52520	Tyrosine aminotransferase	50.05	58
B1	H-X52638	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase	51.92	47

M509 C4	H-X52730	Human gene for phenylethanolamine N-methylase (PNMT) (EC 2.1.1.28)	31.13	35.0kDa
M235 C5	H-X52839	ribosomal protein L17	15.51	18
M426 C2	H-X52943	Human mRNA for ATF-a transcription factor	53.24	64.0kDa
M266 G5	H-X53777	ribosomal protein L23	20.35	31
B4	H-X53961	Lactotransferrin	78.32	78
M462 C6	H-X54150	Fc fragment of IgA, receptor for	31.68	37.0kDa
M302 A6	H-X54304	myosin, light polypeptide 2, regulatory	18.92	32.0kDa
M311 G2	H-X54802	cytochrome-c oxidase, IV subunit	18.7	23.0kDa
M270 H3	H-X54871	guanine nucleotide-binding protein Rab5B, ras-oncogene related [RAB5B], PROTEIN TRANSPORT. PROBABLY INVOLVED IN VESICULAR TRAFFIC (BYSIMILARITY).	23.76	33.0kDa
M313 B6	H-X54936	placenta growth factor [PLGF*]	16.5	22.0kDa
M496 B2	H-X55079	Human lysosomal alpha-glucosidase gene exon 1	104.83	98.0kDa
D1	H-X55330	Aspartylglucosaminidase	38.17	36
E1	H-X55448	H.sapiens G6PD gene for glucose-6-phosphate dehydrogenase	25.41	30
M421 G6	H-X56253	Human MPR46 gene for 46kd mannose 6-phosphate receptor	30.58	52.0kDa
169-89	H-X56468	14-3-3 protein tau	34	27.02
M300 B4	H-X56549	fatty-acid-binding protein, muscle	14.74	17
M298 D2	H-X56740	guanine nucleotide-binding protein rab11 [RAB11*]	23.87	31.0kDa
M266 E5	H-X56932	highly basic protein, 23 kDa	22.44	30.0kDa
M318 G1	H-X57025	insulin-like growth factor I	16.94	18
M305 F5	H-X57348	protein kinase C inhibitor	27.39	35.0kDa
M236 D6	H-X57351	interferon-induced protein 1-8D	14.63	24
H3	H-X57352	interferon-induced protein 1-8U	14.74	38
M305 B6	H-X58079	S-100 protein, alpha chain	10.45	11
E6	H-X59131	H.sapiens D13S106 mRNA for a highly charged amino acid sequene	34.76	50
M248 H5	H-X59268	transcription factor IIB [TCF2B*]	34.87	49
E2	H-X59357	Epstein-Barr virus small RNA-associated protein	14.19	36
M236 D4	H-X59417	macropain, iota subunit , THE INTERACTION OF CALPONIN WITH ACTIN INHIBITS ACTOMYOSIN MG-ATPASE ACTIVITY	27.17	36
M271 H4	H-X59618	ribonucleotide reductase, small subunit	42.9	46

M250 G3	H-X59710	CAAT-box DNA-binding protein, subunit B, CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A [Homo sapiens]	22.66	34
M423 E2	H-X59711	Nuclear transcription factor Y, alpha	38.28	48.0kDa
M271 C7	H-X59798	Cyclin D1 (PRAD1; parathyroid adenomatosis 1). ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S (START) TRANSITION.	32.56	40.0kDa
M270 H5	H-X59834	calmodulin	41.14	53.0kDa
M416 D5	H-X59871	Transcription factor 7 (T-cell specific)	29.59	36.0kDa
M485 D6	H-X60036	Phosphate carrier, mitochondrial	39.82	37.0kDa
M250 D4	H-X60489	translation elongation factor 1, beta	24.86	33.0kDa
F5	H-X60592	Human CDw40 mRNA for nerve growth factor receptor-related B-lymphocyte activation molecule	30.58	46
M312 F3	H-X61587	ras-related rhoG	21.12	21.0kDa
F9	H-X61622	cyclin-dependent kinase 2 [CDK2]	32.89	56
M313 E3	H-X61970	macropain, zeta subunit	26.62	35.0kDa
M428 D1	H-X62055	tyrosine phosphatase, non-receptor type 6	65.78	66.0kDa
M248 C4	H-X62534	high mobility group protein 2, BINDS PREFERENTIALLY SINGLE-STRANDED DNA AND UNWINDS DOUBLE STRANDED DNA.	23.1	37
M305 F3	H-X62753	folate-binding protein	28.38	36
M476 G2	H-X63468	H.sapiens mRNA for transcription factor TFIIE alpha	48.4	53.0kDa
G6	H-X63469	General transcription factor TFIIE beta subunit, 34 kD	32.12	56
G4	H-X63522	H.sapiens mRNA DAUDI6 for retinoic acid X receptor b	58.74	54
M316 G2	H-X63526	translation elongation factor 1, gamma	48.18	52.0kDa
M305 C5	H-X63527	ribosomal protein L19	21.67	33
E2	H-X63629	Cadherin 3 (P-cadherin)	91.3	110
D4	H-X64037-2	General transcription factor IIF, polypeptide 1 (74kD subunit)	56.98	64
M302 C6	H-X64559	tetranectin	22.33	32.0kDa
M271 H1	H-X64728	choroideremia-like [CHML], H.sapiens CHML mRNA	72.27	98
M270 E1	H-X64810	proprotein convertase subtilisin/kexin type 1 [PCSK1], INVOLVED IN PROCESSING OF HORMONE AND OTHER PROTEIN PRECURSORS	82.94	90
M311 F4	H-X64877	complement factor H-related protein	29.81	36.0kDa

M388 D1	H-X65293	protein kinase C, epsilon [PRKCE]	81.18	96.0kDa
B5	H-X65873	kinesin, heavy polypeptide	106.04	34
F4	H-X66079	Spi-B transcription factor (Spi-1/PU.1 related)	28.93	54
F3	H-X66114	2-oxoglutarate carrier protein [OGMT*]	0	37
M305 C6	H-X66141	myosin, light polypeptide 2, regulatory, ventricular	18.37	31
M419 H1	H-X66357	cell division protein kinase 3	33.620	44.0kDa
166-13	H-X66358	serine/threonine-protein kinase KKIALRE	45	39.45
166-25	H-X66360	serine/threonine-protein kinase PCTAIRE-2	60	57.60
M419 A2	H-X66363	serine/threonine-protein kinase PCTAIRE-1	54.600	64.0kDa
166-37	H-X66364	H.sapiens mRNA PSSALRE for serine/threonine protein kinase	38	32.19
M419 B2	H-X66365	cell division protein kinase 6	35.900	46.0kDa
H3	H-X66839	H.sapiens MaTu MN mRNA for p54/58N protein	50.6	54
M266 G3	H-X67325	interferon, alpha-inducible gene p27	13.53	13
M462 H7	H-X67594	Melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	34.98	44.0kDa
M236 C5	H-X67951	Proliferation-associated gene A (natural killer-enhancing factor A), PAGA	22	34
H3	H-X68486	Adenosine receptor A2	45.43	45
M429 E3	H-X68561	Sp4 transcription factor	86.35	86.0kDa
M430 F2	H-X69151	ATP synthase, H ⁺ transporting, subunit C, vacuolar	42.13	58.0kDa
M236 C3	H-X69392	ribosomal protein L26	16.06	29
B3	H-X69532	H.sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exons 1-3	100.32	98
M236 F5	H-X69654	ribosomal protein S26	12.76	18
M421 C8	H-X70218	Protein phosphatase 4 (formerly X), catalytic subunit	33.88	
M266 H5	H-X70848	protein phosphatase 1, alpha catalytic subunit	36.41	37
E1	H-X70940	Eukaryotic translation elongation factor 1 alpha 2	51.04	60
M270 F1	H-X72215	[PIT1], POU domain, class 1, transcription factor 1 (Pit1, growth hormone factor 1)	32.12	40.0kDa
M271 A7	H-X72760	Laminin, beta 2 (laminin S), S-LAMININ IS A LAMININ-LIKE ADHESIVE PROTEIN CONCENTRATED IN THE SYNAPTIC CLEFT OF THE NEUROMUSCULAR JUNCTION.	67.87	75.0kDa

M235 B1	H-X72841	Human retinoblastoma-binding protein (RbAp46) mRNA, complete cds, IEF 7442 (GB:X72841)	46.86	52.0kDa
217-25	H-X73428	DNA-binding protein inhibitor ID-3	20	17.08
M305 B5	H-X73459	signal recognition particle, subunit 14	15.07	20
M250 D6	H-X73460	ribosomal protein L3, isoform 2, COMPONENT OF THE LARGE SUBUNIT OF CYTOPLASMIC RIBOSOMES	44.44	50.0kDa
M462 D8	H-X74008	Protein phosphatase 1, catalytic subunit, gamma isoform	35.64	46.0kDa
M266 G2	H-X74104	Signal sequence receptor, beta; translocon-associated protein, beta subunit	20.24	27
M266 E7	H-X74262	retinoblastoma binding protein RbAp48	46.86	50.0kDa
H1	H-X74330	DNA primase polypeptide 1 (49kD)	46.31	51
M313 F3	H-X74570	gal beta (1-3/1-4) GlcNAc alpha-2,3 sialyltransferase (GB:X74570)	36.3	46.0kDa
M429 H3	H-X74764	H.sapiens mRNA for receptor protein tyrosine kinase	94.120	98.0kDa
M271 E6	H-X75042	V-rel avian reticuloendotheliosis viral oncogene homolog	68.2	88
M305 G2	H-X75252	phosphatidylethanolamine-binding protein	20.68	30
M302 G1	H-X75593	guanine nucleotide-binding protein rab13	22.44	32.0kDa
166-49	H-X75958	H.sapiens trkB mRNA for protein-tyrosine kinase	55	52.54
C4	H-X76013	H.sapiens QRSFs mRNA for glutaminyl-tRNA synthetase	85.36	85
A2	H-X76029	H.sapiens mRNA for neuromedin U	19.25	20
M305 D5	H-X76228	ATP synthase, H ⁺ transporting, subunit E, vacuolar	24.97	36
M298 F6	H-X76648	glutaredoxin	11.77	11.0kDa
M311 A4	H-X76717	metallothionein 11	6.82	14
C4	H-X77533	H.sapiens mRNA for activin type II receptor	56.43	61
H2	H-X77548	H. sapiens cDNA for RFG	67.65	67
169-41	H-X77743	H.sapiens CDK activating kinase mRNA	45	38.1 3
A4	H-X77909	H.sapiens IKBL mRNA	42.02	52
M305 C1	H-X78136	heterogeneous nuclear ribonucleoprotein E2	40.26	40.0kDa
M306 G2	H-X78416	casein, alpha [CSN1]	20.46	33
M271 C2	H-X78678	ketohehexokinase (fructokinase) [KHK], H.sapiens KHK mRNA for ketohehexokinase, clone pHKHK3a	32.89	39

M305 D4	H-X79193	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk- activating kinase) [CDK7]	38.17	35
M431 F2	H-X79389	glutathione S-transferase T1	26.51	34.0kDa
M298 C6	H-X79537	glycogenin	30.8	34.0kDa
M440 C1	H-X79865	H.sapiens Mrp17 mRNA	21.89	31.0kDa
M298 F5	H-X80229	protein kinase PKN	52.8	64.0kDa
167-39	H-X80230	H.sapiens mRNA (clone C-2k) mRNA for serine/threonine protein kinase	42	40.99
217-49	H-X80343	H.sapiens p35 mRNA for regulatory subunit of cdk5 kinase	40	33.84
M270 D7	H-X80695	cytochrome oxidase-assembly protein, OXA1, H.sapiens OXA1Hs mRNA	47.96	50
M266 B5	H-X80909	nascent polypeptide-associate complex, alpha	23.76	37.0kDa
M416 D9	H-X80910	Protein phosphatase 1, catalytic subunit, beta isoform	36.08	45.0kDa
E2	H-X81198	Archain	52.03	63
169-6	H-X81817	H.sapiens BAP31 mRNA	32	27.1 3
E4	H-X82018	H.sapiens mRNA for ZID protein	46.75	57
M313 D7	H-X82456	MLN50	28.82	33
A2	H-X82629	H.sapiens mRNA for Mox-2	33.44	42
M236 D1	H-X83006	lipocalin, neutrophil gelatinase associated	21.89	34.0kDa
166-40	H-X83107	H.sapiens Bmx mRNA for cytoplasmic tyrosine kinase	75	74.32
E3	H-X83425	H.sapiens LU gene for Lutheran blood group glycoprotein	69.19	59
C6	H-X83703	H.sapiens mRNA for cytokine inducible nuclear protein	35.2	54
M416 H2	H-X83928	H.sapiens mRNA for transcription factor TFIID subunit TAFII28	23.32	33.0kDa
166-17	H-X85106	H.sapiens mRNA for ribosomal S6 kinase	90	80.70
166-39	H-X85337	H.sapiens mRNA for myosin light chain kinase	110	109.0
D2	H-X85750	H.sapiens mRNA for transcript associated with monocyte to macrophage differentiation	26.29	30
M266 E6	H-X87176	17-beta-hydroxysteroid dehydrogenase, type 4	81.07	65
M297 F2	H-X87689	CLCP	23.21	33.0kDa
M300 A2	H-X87843	cyclin H assembly factor	34.1	47
M271 E3	H-X89750	homeotic protein, TGIF, H.sapiens mRNA for TGIF protein	30.03	32.0kDa
M235 G1	H-X90529	guanine nucleotide-binding protein ragA [RAGA]	34.54	40
M302 E6	H-X90583	translocon-associated protein, delta	19.14	28.0kDa
M306 G1	H-X90872	gp2512	23.65	33

M416 D2	H-X91504	Transcription factor COUP 2 (a.k.a. ARP1)	22.22	32.0kDa
M250 B3	H-X92098	transmembrane protein rnp24	22.22	30
M271 G7	H-X92106	bleomycin hydrolase. PROTECTING NORMAL AND MALIGNANT CELLS FROM BLM TOXICITY.	50.16	55.0kDa
F3	H-X92715	Zinc finger protein 74 (Cos52)	63.03	47
M270 H6	H-X92720	H.sapiens mRNA for phosphoenolpyruvate carboxykinase	70.51	71
H5	H-X92762	H.sapiens mRNA for tafazzins protein	32.23	37
M298 D3	H-X93036	MAT-8	9.68	16.0kDa
M476 A5	H-X93595	H.sapiens mRNA for NK receptor (clone 17.1C)	50.16	56.0kDa
M417 D2	H-X93920	protein tyrosine phosphatase foreskin	41.980	48.0kDa
A5	H-X95592	H.sapiens mRNA for C1D protein	15.62	28
M298 B4	H-X95648	translation initiation factor 2B, alpha subunit	33.66	34.0kDa
F3	H-X95735	H.sapiens mRNA for zyxin 2	63.03	72
M386 B1	H-X96752	L-3-hydroxyacyl-CoA dehydrogenase, SCHAD gene	34.65	45.0kDa
M422 B6	H-X97229	H.sapiens mRNA for NK receptor, clone library 15.212	41.58	48.0kDa
B3	H-X98173	H.sapiens mRNA for MACH- alpha-2 protein	51.15	51
166-14	H-X99325	H.sapiens mRNA for Ste20-like kinase	55	46.9 3
C4	H-X99459	H.sapiens mRNA for sigma 3B protein	21.34	30
M424 C4	H-Y00291	Human hap mRNA encoding a DNA-binding hormone receptor	49.39	59.0kDa
M386 H1	H-Y00345	polyadenylate-binding protein	69.74	70.0kDa
M469 A2	H-Y00630	Plasminogen activator inhibitor, type II (arginine-serpin)	45.76	46.0kDa
M305 E1	H-Y00711	lactate dehydrogenase B	36.85	38.0kDa
H2	H-Y00764	ubiquinol/cytochrome c reductase hinge protein	10.12	33
F5	H-Y07848	H.sapiens EWS, gar22, rrp22 and bam22 genes	36.3	50
M305 G6	H-Z11559	iron-responsive element binding protein 1 [IREB1]	97.9	98
M250 F3	H-Z11566	Pr22 protein , STATHMIN [Homo sapiens], SERVES AS RELAY (VIA PHOSPHORYLATION) FOR DIVERSE SECOND MESSENGER PATHWAYS	16.5	22.0kDa
169-73	H-Z11695	H.sapiens 40 kDa protein kinase related to rat ERK2	50	38.35
M475 C8	H-Z11737	Flavin-containing monooxygenase 4	61.49	70.0kDa

C1	H-Z11898	Octamer binding protein 3	39.71	50
M266 H4	H-Z12830	SSR, alpha subunit	31.57	42.0kDa
A3	H-Z14000	Ring finger protein 1	41.58	50
M300 E1	H-Z14978	actin-related protein	41.47	49
G1	H-Z19002	H.sapiens of PLZF gene encoding kruppel-like zinc finger protein	74.14	84
H1	H-Z21966	POU homeobox protein	33.22	43
M248 G3	H-Z23139	CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR [Homo sapiens]	29.04	34
D3	H-Z26876	ribosomal protein L38	7.81	35
F2	H-Z28339	H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase	35.97	43
M298 B3	H-Z28407	ribosomal protein L8	28.38	39.0kDa
M313 C3	H-Z29330	ubiquitin-conjugating enzyme UbcH2, 23 kDa	20.24	34
M271 F3	H-Z29677	guanine nucleotide-binding protein, ras-related	20.35	28.0kDa
M465 C2	H-Z30425	H.sapiens mRNA for orphan nuclear hormone receptor	38.39	34.0kDa
M302 F5	H-Z31357	cysteine dioxygenase	22.11	31.0kDa
M340 C1	H-Z31695	inositol polyphosphate 5-phosphatase, 43 kDa	40.04	49.0kDa
E3	H-Z32564-2	H.sapiens FRGAMMA mRNA (819bp) for folate receptor	26.84	36
M236 H1	H-Z35227	small G protein, TTF, RAS-RELATED PROTEIN RAC1	21.12	30.0kDa
A10	H-Z35491	H.sapiens mRNA for novel glucocorticoid receptor-associated protein	30.25	60
M440 G5	H-Z37986	H.sapiens mRNA for phenylalkylamine binding protein	25.41	28.0kDa
M297 E2	H-Z47087	cyclin A/cyclin-dependent kinase 2-associated p19	18.04	30.0kDa
F1	H-Z48051	H.sapiens gene for myelin oligodendrocyte glycoprotein (MOG)	27.28	31
A2	H-Z48475	Glucokinase regulator	68.86	70
M302 E4	H-Z48570	sperm zona pellucida-binding protein	16.72	24
M266 A2	H-Z68907	Human clone ID 193225 NAD (H)-specific isocitrate dehydrogenase gamma subunit mRNA, alternatively spliced, partial cds	43.34	45.0kDa
G1	H-Z83850	Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs	45.76	60

H4	H-Z97171	Homo sapiens GLC1A (trabecular meshwork induced glucocorticoid response) gene, exon I, joined CDS	55.55	55
M421 D5	H-Z97632	Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs	28.49	38.0kDa

Example 3 - Construction of Expression Plasmids

The following example illustrates the construction of the expression vectors used in the Examples above. Similar modifications can be made in other vectors for use in creating libraries of expressible gene sequences.

The vector pcDNA3.1/V5-His was obtained from Invitrogen (cat #V810-20) and modified slightly so that it carried an gene sequence for Zeocin™ resistance and lacked the multiple cloning site. A 100µg aliquot was suspended in 200 µl medical irrigation (MI) water. A 5µl aliquot was saved for gel analysis. The remainder was transferred to a 1.7 ml Eppendorf tube. The vector was digested with HindIII (400 U) using Promega Buffer E (final volume = 400 µl). The reaction ran 3 hours at 37° C. An aliquot was checked for completeness of digestion by running on an 0.8% agarose gel in 1X TAE, and visualizing with ethidium bromide.

The digested vector was treated with 200 µl phenol/chloroform (pH7.5) according to standard procedures, and the DNA precipitated from the aqueous phase using 1/10 volume 3M NaOAc and 2 volumes 100% EtOH at room temperature, followed by washing with 80% EtOH. The pellet was resuspended in 100 µl MI water.

Two oligonucleotides were added to the resuspended DNA (Topo -H (40 µg) 5'-(P)AGCTCGCCCTTATTCCGATAGTG (SEQ ID NO:3), Topo-4 (12 µg) 5'-(P)AGGGCG (SEQ ID NO:4)), plus 17 µl 10X Promega T4 Ligase buffer. The tube was placed on ice and the volume increased to 170 µl with MI water. The oligos were
5 ligated to the vector using 20U Promega T4 DNA ligase, incubated at 12° C overnight.

The vector was treated with 100 µl phenol/chloroform and the aqueous phase precipitated as described above. The pelleted DNA was resuspended in 150 µl of sterile water the redigested with HindIII (17 µl Promega Buffer E, 200 U HindIII - 37°
10 C, 1 hour). The redigested DNA was re-extracted with phenol/chloroform and precipitated with 1/10 volume 3M NaOAc and 7/10 volume isopropanol, then washed with 80% EtOH.

The pelleted DNA was resuspended in 82 µl TE buffer (10 mM Tris, pH 8.0, 1 mM EDTA, pH 8.0). A 2 µl aliquot was used to check the foregoing procedure using
15 agarose gel electrophoresis as described above. The remaining 80 µl was transferred to a Falcon tube and mixed with 16 µg Topo-5 oligonucleotide (5'-(P)CAACACTATCGGAATA (SEQ ID NO:5). To this mixture was added 190 µl NEB Restriction Buffer #1 (room temperature). The total reaction mixture was adjusted to 1.9 mls with MI water. Vaccinia Topoisomerase I enzyme was added (80
20 µg) and the reaction tube placed in a 37° C water bath for 15 minutes.

After 15 minutes, 200 µl of room temperature Topo-10X stop buffer was added (100 mM Tris 7.4, 110 mM EDTA, bromophenol blue). The entire volume was loaded onto an agarose gel (1.2 gr agarose/ 130 mls 1X TAE) and run at 70 volts until the bromophenol blue dye had run down about 1/2 in (volume in the loading well was
25 kept constant by the addition of 1X TE). The voltage was reversed for 90 seconds. The contents of the loading well were transferred to a 15 ml Falcon tube and placed on ice. 2 mls of cold Topo-2X Wash Buffer (60 mM Tris 7.4, 1 mM EDTA, 4 mM dithiothreitol (DTT), 200 µg/ml bovine serum albumin (BSA)) was added and the

volume then adjusted to 4 mls with cold Topo-1X Enzyme Dilution Buffer (50% glycerol, 50 mM Tris 7.4, 1 mM EDTA, 2 mM DTT, 0.1% Triton X-100, 100 µg/ml BSA) plus 4 mls Topo-Glycerol mix (90% glycerol, 10% 50 mM TE pH 7.4, 0.1% Triton X-100) and stored until needed.

- 5 A similar procedure was used to make Topo-adapted pYES2 (Invitrogen cat # V825-20).

 While the foregoing has been presented with reference to particular
embodiments of the invention, it will be appreciated by those skilled in the art that
changes in these embodiments may be made without departing from the principles and
10 spirit of the invention, the scope of which is defined by the appended claims.

That which is claimed is:

1. A method for producing a library of expressible coding regions comprising the steps of:
 - 5 (a) amplifying a plurality of coding regions using at least one coding region specific primer,
 - (b) inserting each coding region into an expression vector, and
 - (c) verifying the size and orientation of the inserted coding region.
2. The method according to claim 1 further comprising transforming cells
10 with the vector containing the verified coding region.
3. The method according to claim 1 further comprising purifying the amplified coding region prior to insertion into an expression vector.
4. The method according to claim 1 wherein the coding regions encode full-length proteins.
- 15 5. The method according to claim 4 wherein the 5' primer used for amplification starts with the nucleotides CACCATG and the 3' primer causes the amplification product to end at the third position of the codon immediately preceding the stop codon of the coding region being amplified plus a single adenine residue.
6. The method according to claim 3 wherein the purification is performed
20 using agarose gel electrophoresis.
7. The method according to claim 6 wherein the agarose is low melt agarose.
8. The method according to claim 1 wherein insertion of the amplified coding region into an expression vector is performed using an enzyme that both cleaves and ligates DNA.

9. The method according to claim 3 wherein the purification is performed using low melt agarose gel electrophoresis and insertion of the amplified coding region into an expression vector is performed using an enzyme that both cleaves and ligates DNA.

5 10. The method according to claim 8 wherein said enzyme is a type I topoisomerase or a site-specific recombinase.

11. The method according to claim 10 wherein said enzyme is vaccinia DNA topoisomerase, lambda integrase, FLP recombinase or P1-Cre protein.

10 12. A method according to claim 11 wherein said enzyme is vaccinia DNA topoisomerase.

13. The method of claim 1 wherein the expression vector is a eukaryotic expression vector.

14. The method of claim 13 wherein said eukaryotic expression vector is pYES2/GS or pcDNA3.1/GS.

15 15. The method of claim 1 wherein the expression vector is a prokaryotic expression vector.

16. The method of claim 15 wherein said prokaryotic expression vector is pBAD.

20 17. The method according to claim 1 wherein the expression vector comprises one or more elements selected from: a promoter-enhancer sequence, a selection marker sequence, an origin of replication, an affinity purification tag sequence, an inducible element sequence and an epitope-tag sequence.

18. The method of claim 1 wherein size and orientation of the insert is verified using a polymerase chain reaction protocol.

19. The method of claim 18 wherein said verification is performed using whole cell lysates.

20. The method of claim 1 wherein the coding regions to be amplified are open reading frame sequences in prokaryotic DNA or eukaryotic DNA.

5 21. The method according to claim 20 wherein the eukaryotic DNA is obtained from yeast or mammalian cells.

22. The method according to claim 1 wherein the coding regions being amplified encode members of a family of proteins.

10 23. The method according to claim 22 wherein the proteins are human proteins.

24. The method according to claim 23 wherein the family of proteins are kinases, phosphatases, transcription factors, oncogenes, or tumor suppressors.

25. The method according to claim 1 wherein steps (a) and (b) are performed in a multiwell microtiter plate.

15 26. The method according to claim 1 wherein coding regions of the correct size and in the correct orientation are robotically selected for transformation into cells for expression.

27. The method according to claim 2 comprising the additional step of verifying that the transformed cells express the coding region.

20 28. The method according to claim 2 wherein the transformed cells are eukaryotic cells or prokaryotic cells.

29. A method according to claim 28 wherein the eukaryotic cells are CHO cells or *S. cerevisiae* cells.

30. An expression library of coding regions produced according to the method of claim 1.
31. The library according to claim 30 wherein the coding regions encode yeast proteins.
- 5 32. The library according to claim 31 wherein the coding regions encode mammalian proteins.
33. The library according to claim 32 wherein the mammalian proteins are human proteins.
- 10 34. The library according to claim 33 wherein the human proteins are kinases, phosphatases, transcription factors, oncogenes, or tumor suppressors.
35. An expression library obtainable from the method of claim 1.
36. An expression vector pYES2/GS.
37. An expression vector pCDNA3.1/GS.

38. A method for producing a library of expressible coding regions comprising the steps of:

- 5 (a) amplifying a plurality of coding regions using PCR, wherein the 5' primer comprises the sequence CACCATG and the 3' primer causes the amplification product to end just prior to any stop codon,
- (b) purifying the amplified coding regions using low melt agarose electrophoresis,
- 10 (c) inserting each of the purified coding regions into an expression vector using vaccinia DNA topoisomerase, wherein said expression vector comprises a promoter-enhancer sequence, a selection marker sequence, an origin of replication, an affinity purification sequence, and an epitope-tag sequence,
- (d) transforming bacterial cells with the insert containing expression vector,
- 15 (e) growing the transformed cells and verifying the size and orientation of the inserted coding region,
- (f) selecting expression vectors containing inserted coding regions in the correct orientation for expression of the gene product, and
- (g) transforming cells for expression with said expression vectors.

1/1

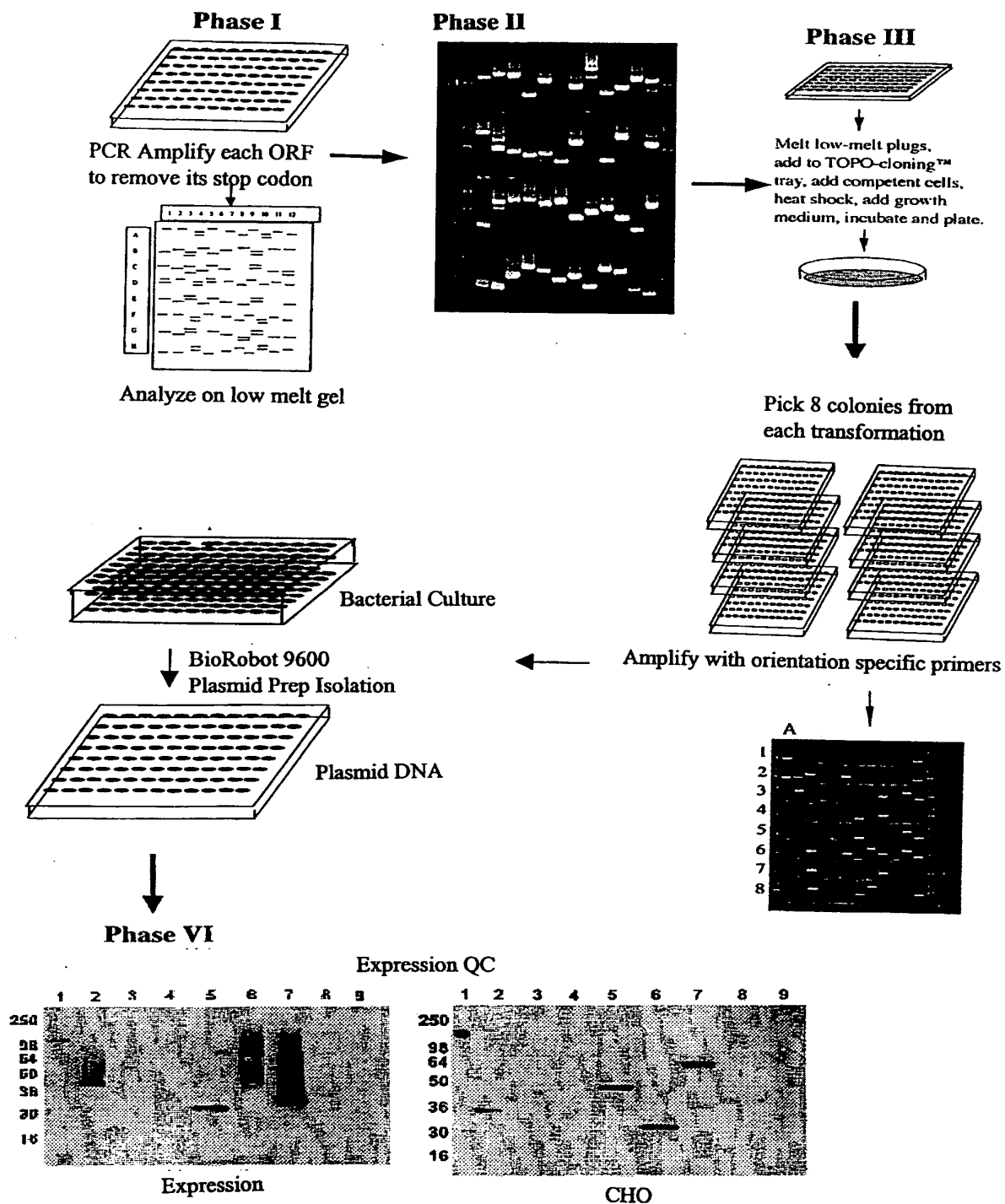


Figure 1
SUBSTITUTE SHEET (RULE 26)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/07270

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) : C12Q 1/6; G01N 33/536, 33/543, 33/53; C07H 21/04 US CL : 435/7.2, 4, 6, 7.23, 21, 320.1; 536/ 23.2, 23.4, 23.5, 24.1 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/7.2, 4, 6, 7.23, 21, 320.1; 536/ 23.2, 23.4, 23.5, 24.1 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) APS, CAS, BIOSIS		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	THIESEN, J. et al. Target detection assay (TDA): a versatile procedure to determine DNA binding sites as demonstrated on SP1 protein. Nucleic Acids Research. 1990, Vol. 18, No. 11, pages 3203-3209, especially 3204.	1-37
Y	SHORE, P. et al. The ETS-domain transcription factors ELK-1 and SAP-1 exhibit differential DNA binding specificities. Nucleic Acids Research. 1995, Vol. 23, No. 22, pages 4698-4706, especially page 4700, col. 1 up to page 4702, col. 2.	1-37
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "B" earlier document published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "Z" document member of the same patent family		
Date of the actual completion of the international search		Date of mailing of the international search report
22 JUNE 1999		02 AUG 1999
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized officer T. WESSENDORF Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/07270

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	NALLUR, G. et al. Multiplex selection technique (MuST): An approach to clone transcription factor binding sites. Proc. Natl. Acad. Sc., USA. February 1996, Vol. 93, pages 1184-1189, especially 1184.	1-37
Y	BAUER, D. et al. Identification of differentially expressed mRNA species by an improved display technique (DDRT-PCR). Nucleic Acids Research. 1993, Vol. 21, No. 18, pages 4272-4280, especially page 4273 up to page 4280.	1-37
Y	US 5,665,578 A (GILLIES) 09 September 1997, abstract.	1-37
A	US 5,432,018 A (DOWER et al) 11 July 1995, col. 12, lines 1-68.	1-38